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OM protein - protein search, using sw model

Run on: February 20, 2002, 12:15:09 : Search time 22.94 Seconds
(without alignments)
63.763 Million cell updates/sec

Title: US-09-724-396-3

Perfect score: 58

Sequence: 1 SMITMWYFDV 10

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Maximum Match 08
Listing first 45 summaries

Database :

SPTREMBL_17:*
1: sp.archaea:*
2: sp.bacteria:*
3: sp.fungi:*
4: sp.human:*
5: sp.invertebrate:*
6: sp.mammal:*
7: sp.mhc:*
8: sp.organelle:*
9: sp.phage:*
10: sp.plant:*
11: sp.podent:*
12: sp.virus:*
13: sp.vertebrate:*
14: sp.unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	48	82.8	74	11	060495
2	48	82.8	160	11	090278
3	45	77.6	484	4	013793
4	45	77.6	587	4	013764
5	45	77.6	607	11	099K32
6	45	77.6	751	13	09DCJ7
7	45	77.6	770	6	09TU10
8	42	72.4	747	13	091963
9	39	67.2	111	5	09VR31
10	39	67.2	474	2	084286
11	39	67.2	474	2	09PKB0
12	38	65.5	194	5	09XVT5
13	38	65.5	376	10	09LS57
14	38	65.5	427	12	09PYT0
15	38	65.5	1398	3	09P3Y3
16	37	63.8	383	10	080505
17	37	63.8	416	5	09NET5
18	37	63.8	431	5	09XT29
19	37	63.8	721	12	090943

20	37	63.8	731	12	0908R8	09g8r myxoma viru
21	37	63.8	848	2	054137	054137 streptomyc
22	37	63.8	5107	5	024498	024498 drosophila
23	36	62.1	125	4	09BV14	09bv14 homo sapien
24	36	62.1	128	4	09NTU9	09ntu9 homo sapien
25	36	62.1	129	4	09BZT0	09bz20 homo sapien
26	36	62.1	236	8	09BBS6	09bbs6 lotus japon
27	36	62.1	325	5	09VN98	09vn98 drosophila
28	36	62.1	374	11	099KX0	099kx0 mus musculu
29	36	62.1	419	11	099KX0	099kx0 mus musculu
30	36	62.1	426	4	09G2T9	09g2t9 homo sapien
31	36	62.1	551	5	09XUB4	09xub4 caenorhabdi
32	36	62.1	596	4	09H1R3	09h1r3 homo sapien
33	36	62.1	617	4	09UFU0	09ufu0 homo sapien
34	36	62.1	617	11	054776	054776 mus musculu
35	36	62.1	638	11	054785	054785 mus musculu
36	36	62.1	733	3	012748	012748 saccharomyc
37	36	62.1	733	4	099464	099464 homo sapien
38	36	62.1	961	10	09FS96	09fs96 saccharum o
39	36	62.1	1019	11	09JHR7	09jhr7 mus musculu
40	36	62.1	3060	5	09YAV4	09yav4 drosophila
41	35	60.3	212	2	043997	043997 anabaena sp
42	35	60.3	222	2	09X1Y6	09x1y6 thermotoga
43	35	60.3	261	5	018875	018875 caenorhabdi
44	35	60.3	335	1	059537	059537 pyrococcus
45	35	60.3	335	1	090XX3	090xx3 pyrococcus

ALIGNMENTS

RESULT 1
ID 060495 PRELIMINARY: PRT: 74 AA.
AC 060495;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN (FRAGMENT).
GN APP.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriognath; Cavidae; Cavia.
OX NCBI_Taxid=10141;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER.
RA Beck M., Mueller D., Bigl V.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC G(O) (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: TO PANCREATIC TRYPSIN INHIBITOR (KUNITZ) DOMAIN.
DR EMBL: X99198; CAA67589.1; -.
DR HSSP: P05067; ITAW.
DR InterPro: IPR002223; Kunitz_BPTI.
DR Pfam: PF00014; Kunitz_BPTI.
DR PRINTS: PR00759; BASICPTASE.
DR SMART: SM00131; KU; 1.
DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE: PS50279; BPTI_KUNITZ_2; 1.
KW Serine protease inhibitor.
FT NON_TER 1
FT NON_TER 74
SQ SEQUENCE 74 AA; 8057 MW; 29AB3407730814D9 CRC64;

Query Match 82.8%; Score 48; DB 11; Length 74;
Best Local Similarity 80.0%; Pred. No. 0.23;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 SMITMWYFDV 10

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DB      13 SMISRWYEDV 22

RESULT  2
ID      090278      PRELIMINARY:      PRT:      160 AA.
AC      090278:
DT      01-MAY-2000 (TREMBlrel. 13, Created)
DT      01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT      01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE      PUTATIVE AMYLOID PRECURSOR PROTEIN (FRAGMENT).
OS      Cavia sp.
OC      Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Hystriognathia; Cavidae; Cavia.
OX      NCBI_TaxID=10143;
RN      11
RP      SEQUENCE FROM N.A.
RC      TISSUE=LENS;
RA      Frederikse P.H., Carper D., Farnsworth J.P., Ziegler J.S.;
RT      "Pitron and Alzheimer precursor protein expression in a hereditary
RT      guinea pig cataract.";
RL      Submitted (OCT-1999) to the EMBL/Genbank/DBJ databases.
CC      -1- SIMILARITY: TO PANCREATIC TRYPsin INHIBITOR (KUNITZ) DOMAIN.
DR      EMBL: AF197164; AAF08934.1; -.
DR      HSSP: P05067; IAAP.
DR      InterPro: IPR002223; Kunitz_BPTI.
DR      Pfam: PF00014; Kunitz_BPTI; 1.
DR      PRINTS: PR00759; BASICPTASE.
DR      SMART: SM00131; KU; 1.
DR      PROSITE: PS00280; BPTI_KUNITZ_1; 1.
DR      PROSITE: PS50279; BPTI_KUNITZ_2; 1.
DR      Serine protease inhibitor.
KW      NON_TER
FT      1
FT      NON_TER
FT      1
SQ      SEQUENCE 160 AA: 17424 MW: 9F28C3E92E7F47C1 CRC64;

Query Match
Best Local Similarity 82.8%; Score 48; DB 11; Length 160;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY      1 SMITNMYEDV 10
DB      78 SMISRWYEDV 87

RESULT  3
ID      013793      PRELIMINARY:      PRT:      484 AA.
AC      013793:
DT      01-NOV-1996 (TREMBlrel. 01, Created)
DT      01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT      01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE      AMYLOID PROTEIN (FRAGMENT).
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX      NCBI_TaxID=9606;
RN      11
RP      SEQUENCE FROM N.A.
RC      TISSUE=BRIN;
RX      MEDLINE=89346754; PubMed=2569763;
RA      de Sauvage F., Octave J.N.;
RT      "A novel mRNA of the A4 amyloid precursor gene coding for a possibly
RT      secreted protein.";
RL      Science 245:651-653(1989).
CC      -1- SIMILARITY: TO PANCREATIC TRYPsin INHIBITOR (KUNITZ) DOMAIN.
DR      EMBL: M28373; AA58727.1; -.
DR      HSSP: P05067; IAAP.
DR      InterPro: IPR001868; A4_APP.
DR      InterPro: IPR002223; Kunitz_BPTI.
DR      Pfam: PF02177; A4_EXTRA; 1.
DR      PRINTS: PR00759; BASICPTASE.
DR      SMART: SM00131; KU; 1.
DR      PROSITE: PS00280; BPTI_KUNITZ_1; 1.
DR      PROSITE: PS50279; BPTI_KUNITZ_2; 1.

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DR      Pfam: PF00014; Kunitz_BPTI; 1.
DR      PRINTS: PR00203; AMYLOIDA4.
DR      PRINTS: PR00759; BASICPTASE.
DR      SMART: SM00006; A4_EXTRA; 1.
DR      SMART: SM00131; KU; 1.
DR      PROSITE: PS00319; A4_EXTRA; 1.
DR      PROSITE: PS00280; BPTI_KUNITZ_1; 1.
DR      PROSITE: PS50279; BPTI_KUNITZ_2; 1.
DR      Amyloid; Glycoprotein; Serine protease inhibitor.
KW      NON_TER
FT      1
FT      NON_TER
FT      1
FT      CARBOHYD
FT      444
FT      444
FT      472
FT      472
SQ      SEQUENCE 484 AA: 54982 MW: CE49DECDE07652A CRC64;

Query Match
Best Local Similarity 77.6%; Score 45; DB 4; Length 484;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY      1 SMITNMYEDV 10
DB      223 AMISRWYEDV 232

RESULT  4
ID      013764      PRELIMINARY:      PRT:      547 AA.
AC      013764:
DT      01-NOV-1996 (TREMBlrel. 01, Created)
DT      01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT      01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE      AMYLOID-BETA PROTEIN.
GN      APP.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX      NCBI_TaxID=9606;
RN      11
RP      SEQUENCE FROM N.A.
RX      MEDLINE=90236318; PubMed=2110105;
RA      Yoshikawa S., Sasaki H., Doh-ura K., Furuya H., Sakaki Y.;
RT      "Genomic organization of the human amyloid beta-protein precursor
RT      gene.";
RL      gene 87:257-263(1990).
RN      12
RP      SEQUENCE FROM N.A.
RA      Yoshikawa K., Izumi R., Oishi N., Sakaki Y.;
RL      Submitted (SEP-1990) to the EMBL/Genbank/DBJ databases.
CC      -1- SIMILARITY: TO PANCREATIC TRYPsin INHIBITOR (KUNITZ) DOMAIN.
DR      EMBL: M34875; AAB59501.1; -.
DR      EMBL: M34862; AAB59501.1; JOINED.
DR      EMBL: M34863; AAB59501.1; JOINED.
DR      EMBL: M34864; AAB59501.1; JOINED.
DR      EMBL: M34865; AAB59501.1; JOINED.
DR      EMBL: M34866; AAB59501.1; JOINED.
DR      EMBL: M34867; AAB59501.1; JOINED.
DR      EMBL: M34868; AAB59501.1; JOINED.
DR      EMBL: M34869; AAB59501.1; JOINED.
DR      EMBL: M34870; AAB59501.1; JOINED.
DR      EMBL: M34871; AAB59501.1; JOINED.
DR      EMBL: M34872; AAB59501.1; JOINED.
DR      EMBL: M34873; AAB59501.1; JOINED.
DR      HSSP: P05067; IMWP.
DR      InterPro: IPR001868; A4_APP.
DR      InterPro: IPR002223; Kunitz_BPTI.
DR      Pfam: PF02177; A4_EXTRA; 1.
DR      Pfam: PF00014; Kunitz_BPTI; 1.
DR      PRINTS: PR00759; BASICPTASE.
DR      SMART: SM00006; A4_EXTRA; 1.
DR      SMART: SM00131; KU; 1.
DR      PROSITE: PS00319; A4_EXTRA; 1.
DR      PROSITE: PS00280; BPTI_KUNITZ_1; 1.
DR      PROSITE: PS50279; BPTI_KUNITZ_2; 1.

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KM Serine protease inhibitor.
SQ SEQUENCE 547 AA; 62135 MW; DB1BJE0FF22D2070 CRC64;

Query Match 77.6%; Score 45; DB 4; Length 547;
Best Local Similarity 70.0%; Pred. No. 5.5;

Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 SMITNWFYEDV 10
DB 302 AMISRWYEDV 311

RESULT 5

Q99K32 PRELIMINARY; PRT; 607 AA.

ID Q99K32
AC Q99K32;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE UNKNOWN (PROTEIN FOR IMAGE:3486773) (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=MAMMARY TUMOR;
RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
FT EMBL; BC005490; AA05490.1;
FT NON TER 1
SQ SEQUENCE 607 AA; 68391 MW; BF80221CBA7D172 CRC64;

Query Match 77.6%; Score 45; DB 11; Length 607;
Best Local Similarity 70.0%; Pred. No. 6.1;

Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 SMITNWFYEDV 10
DB 139 AMISRWYEDV 148

RESULT 6

Q9DGI7 PRELIMINARY; PRT; 751 AA.

ID Q9DGI7
AC Q9DGI7;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE BETA-AMYLOID PRECURSOR PROTEIN 751 ISOFORM.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Sarasa M., Rodolase A., Sorribas V.;
RT "Cloning of full-length chicken beta-amyloid precursor protein
RT isoforms."
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: TO PANCREATIC TRYPsin INHIBITOR (KUNITZ) DOMAIN.
EMBL; AF289219; AAC00594.1;
DR InterPro: IPR001868; A4_APP.
DR InterPro: IPR002223; Kunitz_BPTI.
DR Pfam: PF02177; A4_EXTRA; 1.
DR Pfam: PF00014; Kunitz_BPTI; 1.
DR PRINTS: PR00203; AMYLOIDA.
DR PRINTS: PR00759; BASICTASE.
DR SMART: SM00006; A4_EXTRA; 1.
DR SMART: SM00131; KU; 1.

DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE: PS50279; BPTI_KUNITZ_2; 1.
KM Serine protease inhibitor.
SQ SEQUENCE 751 AA; 84705 MW; E78E9413A8033084 CRC64;

Query Match 77.6%; Score 45; DB 13; Length 751;
Best Local Similarity 70.0%; Pred. No. 7.6;

Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 SMITNWFYEDV 10
DB 302 AMISRWYEDV 311

RESULT 7

Q9TU10 PRELIMINARY; PRT; 770 AA.

ID Q9TU10
AC Q9TU10;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE AMYLOID PRECURSOR PROTEIN.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.
OX NCBI_TaxID=9623;
RN [1]
RP SEQUENCE FROM N.A.
RA Kimura A., Takahashi T.;
RT "Amyloid Precursor Protein 770."
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: TO PANCREATIC TRYPsin INHIBITOR (KUNITZ) DOMAIN.
EMBL; AB032550; BAA64380.1;
DR HSP; P05067; IAP.
DR InterPro: IPR001868; A4_APP.
DR InterPro: IPR002223; Kunitz_BPTI.
DR Pfam: PF02177; A4_EXTRA; 1.
DR Pfam: PF00014; Kunitz_BPTI; 1.
DR PRINTS: PR00203; AMYLOIDA.
DR PRINTS: PR00759; BASICTASE.
DR SMART: SM00006; A4_EXTRA; 1.
DR SMART: SM00131; KU; 1.
DR PROSITE: PS00319; A4_EXTRA; 1.
DR PROSITE: PS00320; A4_INTRA; 1.
DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE: PS50279; BPTI_KUNITZ_2; 1.
KM Serine protease inhibitor.
SQ SEQUENCE 770 AA; 86961 MW; 5F7A1DCB2BCC583E CRC64;

Query Match 77.6%; Score 45; DB 6; Length 770;
Best Local Similarity 70.0%; Pred. No. 7.8;

Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 SMITNWFYEDV 10
DB 302 AMISRWYEDV 311

RESULT 8

Q91963 PRELIMINARY; PRT; 747 AA.

ID Q91963
AC Q91963;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE AP747.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipiloidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;

RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93129227; PubMed=1282805;
 RA Okada H., Okamoto H.;
 RT "A Xenopus homolog of the human beta-amyloid precursor protein:
 RL developmental regulation of its gene expression";
 CC Blochem. Biophys. Res. Commun. 189:1561-1568(1992).
 DR EMBL; S52417; AB24853.1; -
 DR HSSP; P05067; 10CM.
 DR InterPro: IPR001868; A4_APP.
 DR InterPro: IPR002223; Kunitz_BPTI.
 DR Pfam: PF02177; A4_EXTR1.
 DR Pfam: PF00014; Kunitz_BPTI.1.
 DR PRINTS; PR00203; AMYLOIDA.
 DR PRINTS; PR00759; BASICPTASE.
 DR SMART; SM00006; A4_EXTRA.1.
 DR SMART; SM00131; KU; 1.
 DR PROSITE; PS00319; A4_EXTRA.1.
 DR PROSITE; PS00320; A4_INTRA.1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.
 KM Serine protease inhibitor.
 SO SEQUENCE 747 AA; 84892 MW; A75E8185681D948 CRC64;

Query Match 72.4%; Score 42; DB 13; Length 747;
 Best Local Similarity 60.0%; Pred. No. 25;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 SMITMYEYV 10
 DB 298 AMISRYDYV 307

RESULT 9
 Q9VE31 PRELIMINARY; PRT; 111 AA.
 AC Q9VE31.
 DT 01-MAY-2000 (TRENBLrel. 13, Created)
 DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)
 DE CG14298 PROTEIN.
 GN CG14298.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champagne M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abell J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktoglu L., Beasley E.M.,
 RA Beeson K.T., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Bockova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,
 RA Burlis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Fertiera S., Fleischmann W.,
 RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostlin D., Houston K.A., Howland T.J., Mei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Ruskern D.R., Pateb J.M.,
 RA Palazolo M., Peltman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Relvert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svrtens R., Teator C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster."
 RL Science 287:2185-2195(2000).
 CC -1- SIMILARITY: TO PANCREATIC TRYPsin INHIBITOR (KUNITZ) DOMAIN.
 DR EMBL; AE003724; AAF5559.1; -.
 DR HSSP; P05067; 17AM.
 DR FlyBase; FBgn0038654; CG14298.
 DR InterPro: IPR002223; Kunitz_BPTI.
 DR Pfam: PF00014; Kunitz_BPTI.1.
 DR PRINTS; PR00759; BASICPTASE.
 DR SMART; SM00131; KU; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.
 KM Serine protease inhibitor.
 SO SEQUENCE 111 AA; 12245 MW; 46D06060B79BC678 CRC64;

Query Match 67.2%; Score 39; DB 5; Length 111;
 Best Local Similarity 62.5%; Pred. No. 12;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 MITNMYED 9
 DB 73 VYTRMYED 80

RESULT 10
 O84286 PRELIMINARY; PRT; 474 AA.
 AC O84286;
 DT 01-NOV-1998 (TRENBLrel. 08, Created)
 DT 01-NOV-1998 (TRENBLrel. 08, Last sequence update)
 DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)
 DE PHOSPHOLIPASE D SUPERFAMILY.
 GN CT284.
 OS Chlamydia trachomatis.
 OC Bacteria; Chlamydiales; Chlamydiales; Chlamydia.
 OX NCBI_TaxID=813;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=D/WR-3/CX;
 RX MEDLINE=99000609; PubMed=9784136;
 RA Stephens R.S., Kaiman S., Lammel C.J., Fan J., Marathe R., Aravind L.,
 RA Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,
 RA Davis R.W.;
 RT "Genome sequence of an obligate intracellular pathogen of humans:
 RL Chlamydia trachomatis."
 RL Science 282:754-759(1998).
 DR EMBL; AE001301; AAC67877.1; -
 DR InterPro: IPR001736; PLD.
 DR Pfam; PF00614; PLDC.2.
 DR SMART; SM00155; PLDC.2.
 KM Complete Proteome.
 SO SEQUENCE 474 AA; 54315 MW; 3A189P9718FA4319 CRC64;

Query Match 67.2%; Score 39; DB 2; Length 474;
 Best Local Similarity 85.7%; Pred. No. 53;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 3 ITNMYFD 9
 |||||
 Db 452 ITNMYFD 458

RESULT 11

O9PKB0 PRELIMINARY: PRT: 474 AA.
 ID 09PKB0; PRT: 474 AA.
 AC 09PKB0;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE PHOSPHOLIPASE D FAMILY PROTEIN.
 GN TC0557.
 OS Chlamydia muridarum.
 OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
 OX NCBI_TaxID=83560;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-MOPN / NIGG;
 RX MEDLINE=20150235; PubMed=10684935;
 RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
 RA White O., Hickey E.K., Peterson J., Uterback T., Berry K., Bass S.,
 RA Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
 RA Gwin M., Nelson M., Deboy R., Kolonay J., McClarty G., Salzberg S.L.,
 RA Eisen J., Fraser C.M.;
 RT "Genome sequences of Chlamydia trachomatis Mopn and Chlamydia
 pneumoniae AR39."
 RL Nucleic Acids Res. 28:1397-1406(2000).
 DR EMBL: AE002324; AAF39396.1;
 DR TIGR: TC0557;
 DR InterPro: IPR001736; PLD.
 DR Pfam: PF00614; PLDC; 2.
 DR Complete proteome.
 KW SEQUENCE 474 AA; 54170 MW; 9A4C506FOAB8242 CRC64;
 SO

Query Match

Best Local Similarity 85.7%; Score 39; DB 2; Length 474;
 Pred. No. 53;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 3 ITNMYFD 9
 |||||
 Db 452 ITNMYFD 458

RESULT 12

O9XVT5 PRELIMINARY: PRT: 194 AA.
 ID 09XVT5;
 AC 09XVT5;
 DT 01-NOV-1999 (TREMBlrel. 12, Created)
 DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
 DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
 DE C15C6.1 PROTEIN.
 GN C15C6.1.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidae;
 OC Rhabditidae; Pelodierinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC Kershaw J.;
 RL Submitted (OCT-1996) to the EMBL/GenBank/DDJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94150718; PubMed=7906398;
 RA Wilson R., Almscough R., Anderson K., Baynes C., Berts M.,
 RA Bonfield J., Burton S., Connell M., Copsey J., Coulson A.,
 RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
 RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
 RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,

RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
 RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Showkneen R.,
 RA Smalton N., Smith A., Sonhammer E., Staden R., Sulston J.,
 RA Thierley-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
 RA Watson A., Weinstein L., Wilkinson-Sproat J., Wohlman P.;
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 elegans."
 RT elegans."
 RL Nature 368:32-38(1994).
 DR EMBL: Z81034; CAB02726.1;
 SO SEQUENCE 194 AA; 22700 MW; 308459B673CECDC8 CRC64;

Query Match
 Best Local Similarity 65.5%; Score 38; DB 5; Length 194;
 Pred. No. 32;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 MITNMYFD 9
 ||:| |
 Db 120 MISNMYFD 127

RESULT 13

O9LS57 PRELIMINARY: PRT: 376 AA.
 ID 09LS57;
 AC 09LS57;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE GB|AAC69119.1.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-COLUMBIA;
 RA Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Tabata S.;
 RL Submitted (Apr-1999) to the EMBL/GenBank/DDJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-COLUMBIA;
 RX MEDLINE=20277480; PubMed=10819329;
 RA Nakamura Y.;
 RT "Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence
 features of the regions of 4,504,864 bp covered by sixty P1 and TAC
 clones."
 RL DNA Res. 7:131-135(2000).
 DR EMBL: AB026658; BAB01099.1;
 DR InterPro: IPR001810; F-box.
 DR Pfam: PF00646; F-box; 1.
 DR SMART: SM00256; FBOX; 1.
 DR PROSITE: PS50181; FBOX; 1.
 SO SEQUENCE 376 AA; 43314 MW; A3BB96811783DC78 CRC64;

Query Match

Best Local Similarity 65.5%; Score 38; DB 10; Length 376;
 Pred. No. 62;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 2 MITNMYFD 9
 :: |||||
 Db 189 ILPNMYFD 196

RESULT 14

O9PYT0 PRELIMINARY: PRT: 427 AA.
 ID 09PYT0;
 AC 09PYT0;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE ORF114.

GN ORF14.
 OS Xestia c-nigrum granulosis virus (Xncv) (Xestia c-nigrum
 OS granulovirus).
 OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae; Granulovirus.
 OX NCBI_TaxID=51677;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99434230; PubMed=10502508;
 RA Hayakawa T., Ko R., Okano K., Seong S.I., Goto C., Maeda S.;
 RT "Sequence analysis of the Xestia c-nigrum granulovirus genome.";
 RL Virology 262:277-297(1999).
 DR EMBL: AF162221; AAF05228.1;
 SO SEQUENCE 427 AA; 49747 MW; DA3412CC416207AC CRC64;

Query Match 65.5%; Score 38; DB 12; Length 427;
 Best Local Similarity 55.6%; Pred. NO. 71;
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 2 ITNNWYFDV 10
 : : : : :
 Db 149 WVRNWLFDI 157

RESULT 15
 ID Q9P3Y3 PRELIMINARY; PRT; 1398 AA.
 AC Q9P3Y3;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE ALPHA-AMINOADIPATE REDUCTASE (EC 1.2.1.31).
 GN Lys2.
 OS Pichia farinosa (Yeast).
 CC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Pichia.
 OX NCBI_TaxID=4920;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CBS 7064;
 RA Bleykasten-Grosshans C., Prior C., Potler S.;
 RT "Cloning and sequence of the LYS2 homologue gene from the osmotolerant
 RT yeast Pichia sorbitophila.";
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AJ288950; CAB97252.1;
 DR InterPro: IPR000873; AMP-bind.
 DR Pfam: PF00501; AMP-binding.1.
 DR Pfam: PF00550; PP-binding.1.
 DR PROSITE: PS50075; ACP_DOMAIN.1.
 DR PROSITE: PS00455; AMP_BINDING.1.
 DR PROSITE: PS00012; PHOSPHOPANTHETHEINE; UNKNOWN.1.
 KW Oxidoreductase; Phosphopantetheine.
 SO SEQUENCE 1398 AA; 155776 MW; 791381FE3AF8D020 CRC64;

Query Match 65.5%; Score 38; DB 3; Length 1398;
 Best Local Similarity 85.7%; Pred. NO. 2.3e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 3 ITNNWYFD 9
 : : : : :
 Db 646 ITNNWYVD 652

Search completed: February 20, 2002, 12:16:50
 Job time: 101 sec

FT DISULFID 28 49 BY SIMILARITY

FT NON_TER 76 76
SQ SEQUENCE 76 AA: 8527 MW: 492BF3069AB082A1 CRC64;
Query Match 77.6%; Score 45; DB 1; Length 76;
Best Local Similarity 70.0%; Pred. No. 0.21;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
OY 1 SMITMWFDV 10
:11:11111
DB 14 AMISRWFDV 23

RESULT 2
A4_MACEFA STANDARD: PRT: 87 AA.
ID A4_MACEFA
AC P53601:
DT 01-OCT-1996 (Rel. 34, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN (FRAGMENT).
GN APP.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91273117; PubMed=1905108;
RA Podlasky M.B., Tolan D.R., Selkoe D.J.:
RT "Homology of the amyloid beta protein precursor in monkey and human
RT supports a plimete model for beta amyloidosis in Alzheimer's
RT disease."
RL Am. J. Pathol. 138:1423-1435(1991).
CC -1- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC G(O).
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- ALTERNATIVE PRODUCTS: 5 ISOFORMS: APP(395), APP(563), APP(695),
CC APP(751) AND APP(770) (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE
CC SPLICING (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -1- SIMILARITY: CONTAINS 1 BPTI/KUNITZ INHIBITOR DOMAIN.
CC
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CC
CC EMBL: M58726; AAA36828.1; -;
DR InterPro: IPR001868; A4_APP.
DR InterPro: IPR002223; Kunitz_BPTI.
DR Pfam: PF00014; Kunitz_BPTI.1.
DR PRINTS: PR00759; BASICPTASE.
DR SMART: SM00131; KU; 1.
DR PROSITE: PS00319; A4_EXTRA: PARTIAL.
DR PROSITE: PS00320; A4_INTRA: PARTIAL.
DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE: PS50279; BPTI_KUNITZ_2; 1.
KW Glycoprotein; Amyloid; Neurone; Alternative splicing;
KW Serine protease inhibitor.
FT DOMAIN 1 1
FT NON_TER 4 79
FT ACT_SITE 16 17 BPTI/KUNITZ INHIBITOR.
FT DISULFID 6 36 REACTIVE BOND.
FT DISULFID 15 39 BY SIMILARITY.
FT DISULFID 31 52 BY SIMILARITY.
FT NON_TER 87 87
SQ SEQUENCE 87 AA: 9608 MW: B67C690DEDEE7FF CRC64;

Query Match 77.6%; Score 45; DB 1; Length 87;
Best Local Similarity 70.0%; Pred. No. 0.24;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
OY 1 SMITMWFDV 10
:11:11111
DB 17 AMISRWFDV 26

RESULT 3
A4_SAISC STANDARD: PRT: 751 AA.
ID A4_SAISC
AC Q95241:
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN PRECURSOR [CONTAINS: BETA-
DE AMYLOID PROTEIN (BETA-APP) (A-BETA)].
GN APP.
OS Saimiri sciureus (Common squirrel monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Cebinae; Saimiri.
OX NCBI_TaxID=9521;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver, and Kidney;
RX MEDLINE=96108492; PubMed=8532114;
RA Levy E., Amorim A., Frangione B., Walker L.C.:
RT "Beta-amyloid precursor protein gene in squirrel monkeys with
RT cerebral amyloid angiopathy."
RL Neurobiol. Aging 16:805-808(1995).
CC -1- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC G(O).
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL FOR ITS ASSOCIATION
CC WITH X11-ALPHA, -BETA, AND -GAMMA. THE SEQUENCE SPECIFIC
CC RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL TO THE
CC NPXY MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF
CC PHOSPHORYLATION (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -1- SIMILARITY: CONTAINS 1 BPTI/KUNITZ INHIBITOR DOMAIN.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: S81024; A0D14347.1; -;
DR InterPro: IPR001868; A4_APP.
DR InterPro: IPR002223; Kunitz_BPTI.
DR Pfam: PF02177; A4_EXTRA: 1.
DR Pfam: PF00014; Kunitz_BPTI.1.
DR PRINTS: PR00203; AMYLOIDA4.
DR PRINTS: PR00204; BETAAMYLOID.
DR PRINTS: PR00759; BASICPTASE.
DR SMART: SM00006; A4_EXTRA: 1.
DR SMART: SM00131; KU; 1.
DR PROSITE: PS00319; A4_EXTRA: 1.
DR PROSITE: PS00320; A4_INTRA: 1.
DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE: PS50279; BPTI_KUNITZ_2; 1.
KW Glycoprotein; Amyloid; Neurone; Transmembrane; Alternative splicing;
KW Signal; Serine protease inhibitor.
FT SIGNAL 1 17
FT CHAIN 18 751 A4 PROTEIN.
FT CHAIN 653 695 BETA-AMYLOID PROTEIN (POTENTIAL).
FT DOMAIN 18 680 EXTRACELLULAR (POTENTIAL).
FT

FT TRANSMEM 681 704 POTENTIAL.
 FT DOMAIN 705 751 CYTOPLASMIC (POTENTIAL).
 FT SITE 287 345 BPTI/KUNITZ INHIBITOR.
 FT ACT_SITE 740 743 CLATHRIN-BINDING (BY SIMILARITY).
 FT DISULFID 301 302 REACTIVE BOND.
 FT DISULFID 291 341 BY SIMILARITY.
 FT DISULFID 300 324 BY SIMILARITY.
 FT CARBOHYD 316 337 BY SIMILARITY.
 FT CARBOHYD 523 523 N-LINKED (GLCNAC. . .) (PROBABLE).
 FT SEQUENCE 552 552 N-LINKED (GLCNAC. . .) (PROBABLE).
 SQ SEQUENCE 751 AA: 84893 MW: 6C3FA31089569049 CRC64;

Query Match 77.6%; Score 45; DB 1; Length 751;
 Best Local Similarity 70.0%; Pred. No. 2.1;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 SMITNWPEDV 10
 :||:||||
 Db 302 AMISRWYFDV 311

RESULT 4
 A4_HUMAN STANDARD: PRT: 770 AA.
 ID A4_HUMAN
 AC P05067; P09000; Q16011;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 01-NOV-1991 (Rel. 20, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN PRECURSOR (PROTEASE NEXIN-II)
 DE (NP-II) (APP) [CONTAINS: BETA-AMYLOID PROTEIN (BETA-APP) (A-BETA)].
 GN APP OR A4 OR CVAP OR ADL.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Brain;
 RX MEDLINE=87144572; PubMed=2881207;
 RA Kang J., Lemaire H.-G., Unterbeck A., Salbaum J.M., Masters C.L.,
 RA Grieschik K.-H., Multhaup G., Beyreuther K., Mueller-Hill B.;
 RT "The precursor of Alzheimer's disease amyloid A4 protein resembles a
 RT cell-surface receptor.";
 RL Nature 325:733-736(1987).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88122639; PubMed=2893289;
 RA Ponte P., Gonzalez-Dewhitt P., Schilling J., Miller J., Hsu D.,
 RA Greenberg B., Davis K., Wallace W., Lieberburg I., Fuller F.,
 RA Cordell B.;
 RT "A new A4 amyloid mRNA contains a domain homologous to serine
 RT proteinase inhibitors.";
 RL Nature 331:525-527(1988).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89128427; PubMed=2783775;
 RA Lemaire H.G., Salbaum J.M., Multhaup G., Kang J., Bayney R.M.,
 RA Unterbeck A., Beyreuther K., Mueller-Hill B.;
 RT "The Pread(695) precursor protein of Alzheimer's disease A4 amyloid
 RT is encoded by 16 exons.";
 RL Nucleic Acids Res. 17:517-522(1989).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97263807; PubMed=9108164;
 RA Hattori M., Tsukahara F., Furuhata Y., Tanahashi H., Hirose M.,
 RA Saito M., Tsukuni S., Sakaki Y.;
 RT "A novel method for making nested deletions and its application for
 RT sequencing of a 300 kb region of human APP locus.";
 RL Nucleic Acids Res. 25:1802-1808(1997).
 RN [5]
 RP SEQUENCE OF 286-345 AND 365-366 FROM N.A.
 RX MEDLINE=88122640; PubMed=2893290;

RA Tanzi R.E., McClatchey A.I., Lamperti E.D., Villa-Komaroff L.,
 RA Gusella J.F., Neve R.L.;
 RT "Protease inhibitor domain encoded by an amyloid protein precursor
 RT mRNA associated with Alzheimer's disease.";
 RL Nature 331:528-530(1988).
 RN [6]
 RP SEQUENCE OF 287-367 FROM N.A.
 RX MEDLINE=88122641; PubMed=2893291;
 RA Kitaguchi N., Takahashi Y., Tokushima Y., Shiojiri S., Ito H.;
 RT "Novel precursor of Alzheimer's disease amyloid protein shows
 RT protease inhibitory activity.";
 RL Nature 331:530-532(1988).
 RN [7]
 RP SEQUENCE OF 284-289 AND 365-770 FROM N.A.
 RX MEDLINE=87231971; PubMed=3035574;
 RA Robakis N.K., Ramakrishna N., Wolfe G., Wisniewski H.M.;
 RT "Molecular cloning and characterization of a cDNA encoding the
 RT cerebrovascular and the neuritic plaque amyloid peptides.";
 RL Proc. Natl. Acad. Sci. U.S.A. 84:4190-4194(1987).
 RN [8]
 RP SEQUENCE OF 507-770 FROM N.A.
 RX MEDLINE=88124954; PubMed=2893379;
 RA Zain S.B., Salim M., Chou W.G., Sajdel-Sulkowska E.M., Majocha R.E.,
 RA Marotta C.A.;
 RT "Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer
 RT disease brain: coding and noncoding regions of the fetal precursor
 RT mRNA are expressed in the cortex.";
 RL Proc. Natl. Acad. Sci. U.S.A. 85:929-933(1988).
 RN [9]
 RP SEQUENCE OF 672-681.
 RX MEDLINE=88035004; PubMed=3312495;
 RA Pardridge W.M., Vinters H.V., Yang J., Eisenberg J., Choi T.B.,
 RA Tourtellotte W.W., Huebner V., Shively J.E.;
 RT "Amyloid angiopathy of Alzheimer's disease: amino acid composition
 RT and partial sequence of a 4,200-dalton peptide isolated from cortical
 RT microvessels.";
 RL J. Neurochem. 49:1394-1401(1987).
 RN [10]
 RP SEQUENCE OF 739-770 FROM N.A.
 RX MEDLINE=90236318; PubMed=2110105;
 RA Yoshikai S.-I., Sasaki H., Doh-ura K., Furuya H., Sakaki Y.;
 RT "Genomic organization of the human amyloid beta-protein precursor
 RT gene.";
 RL Gene 87:257-263(1990).
 RN [11]
 RP SEQUENCE OF 1-10 FROM N.A.
 RC TISSUE-Liver;
 RX MEDLINE=89016647; PubMed=3140222;
 RA Schon E.A., Mita S., Sadlock J., Herbert J.;
 RT "A cDNA specifying the human amyloid beta precursor protein (ABPP)
 RT encodes a 95-kDa polypeptide.";
 RL Nucleic Acids Res. 16:9351-9351(1988).
 RN [12]
 RP SEQUENCE OF 18-50.
 RX MEDLINE=87250462; PubMed=3597385;
 RA van Nostrand W.E., Cunningham D.D.;
 RT "Purification of protease nexin II from human fibroblasts.";
 RL J. Biol. Chem. 262:8508-8514(1987).
 RN [13]
 RP IDENTITY OF APP WITH NEXIN-II.
 RX MEDLINE=89384866; PubMed=2506449;
 RA Oltersdorf T., Fritz L.C., Schenk D.B., Lieberburg I.,
 RA Johnson-Wood K.L., Beattie E.C., Ward P.J., Blacher R.W., Dovey H.F.,
 RA Sinha S.;
 RT "The secreted form of the Alzheimer's amyloid precursor protein with
 RT the Kunitz domain is protease nexin-II.";
 RL Nature 341:144-147(1989).
 RN [14]
 RP PROTEASE-SPECIFICITY OF INHIBITOR DOMAIN.
 RX MEDLINE=90211252; PubMed=1969731;
 RA Kido H., Fukuiomi A., Schilling J., Wang Y., Cordell B., Katunuma N.;
 RT "Protease-specificity of Kunitz inhibitor domain of Alzheimer's
 RT disease amyloid protein precursor.";

RL Biochem. Biophys. Res. Commun. 167:716-721(1990).
 RN [15]
 RP COMPLEX WITH G(O).
 RX MEDLINE-9318965; Pubmed-8446172;
 RA Nishimoto I., Okamoto T., Mutsura Y., Takahashi S., Okamoto T.,
 RA Murayama Y., Oota E.;
 RT "Alzheimer amyloid protein precursor complexes with brain GTP-binding
 RT protein G(O).";
 RL Nature 362:75-79(1993).
 RN [16]
 RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 28-133.
 RX MEDLINE-99215582; Pubmed-10201399;
 RA Rossjohn J., Cappai R., Fell S.C., Henry A., McKinstry W.J.,
 RA Galatis D., Hesse L., Multhaup G., Beyreuther K., Masters C.L.,
 RA Parker M.W.;
 RT "Crystal structure of the N-terminal, growth factor-like domain of
 RT Alzheimer amyloid precursor protein.";
 RL Nat. Struct. Biol. 6:327-331(1999).
 RN [17]
 RP X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS) OF 287-344.
 RX MEDLINE-91104913; Pubmed-2123487;
 RA Hynes T.R., Randal M., Kennedy L.A., Eigenbrodt C., Kossakof A.A.;
 RT "X-ray crystal structure of the protease inhibitor domain of
 RT Alzheimer's amyloid beta-protein precursor.";
 RL Biochemistry 25:10018-10022(1990).
 RN [18]
 RP STRUCTURE BY NMR OF 289-344.
 RX MEDLINE-9201468; Pubmed-1718421;
 RA Heald S.L., Tilton R.F. Jr., Hammond L.S., Lee A., Bayney R.M.,
 RA Kamarch M.E., Ramabhadran T.V., Dreyer R.N., Davis G., Unterbeck A.,
 RA Tamburini P.P.;
 RT "Sequential NMR resonance assignment and structure determination of
 RT the Kunitz-type inhibitor domain of the Alzheimer's beta-amyloid
 RT precursor protein.";
 RL Biochemistry 30:10467-10478(1991).
 RN [19]
 RP STRUCTURE BY NMR OF 672-699.
 RX MEDLINE-94281210; Pubmed-7516706;
 RA Talarous J., Marchowski K.J., Klopman G., Zagorski M.G.;
 RT "Solution structure of residues 1-28 of the amyloid beta-peptide.";
 RL Biochemistry 33:7788-7796(1994).
 RN [20]
 RP STRUCTURE BY NMR OF 696-706.
 RX MEDLINE-97128622; Pubmed-8973180;
 RA Kohno T., Kobayashi K., Maeda T., Sato K., Takashima A.;
 RT "Three-dimensional structures of the amyloid beta peptide (25-35) in
 RT membrane-mimicking environment.";
 RL Biochemistry 35:16094-16104(1996).
 RN [21]
 RP STRUCTURE BY NMR OF 672-711.
 RX MEDLINE-98359783; Pubmed-9693002;
 RA Coles M., Bicknell W., Watson A.A., Falrlie D.P., Craik D.J.;
 RT "Solution structure of amyloid beta-peptide(1-40) in a water-miscelle
 RT environment. Is the membrane-spanning domain where we think it is?";
 RL Biochemistry 37:11064-11077(1998).
 RN [22]
 RP STRUCTURE BY NMR OF 672-699.
 RX MEDLINE-20400066; Pubmed-10940222;
 RA Poulsen S.A., Watson A.A., Craik D.J.;
 RT "Solution structures in aqueous SDS micelles of two amyloid beta
 RT peptides of Abeta(1-28) mutated at the alpha-secretase cleavage
 RT site.";
 RL J. Struct. Biol. 130:142-152(2000).
 RN [23]
 RP SIGNAL SEQUENCE CLEAVAGE SITE, AND TOPOLOGY.
 RX MEDLINE-88296437; Pubmed-2900137;
 RA Dyke T., Weidmann A., Multhaup G., Salbaum J.M., Lemaire H.-G.,
 RA Kang J., Mueller-Hill B., Masters C.L., Beyreuther K.;
 RT "Identification, transmembrane orientation and biogenesis of the
 RT amyloid A4 precursor of Alzheimer's disease.";
 RL EMBO J. 7:949-957(1988).
 RN [24]
 RP REVIEW.

RX MEDLINE-92271194; Pubmed-1589757;
 RA Kosik K.S.;
 RT "Alzheimer's disease: a cell biological perspective.";
 RL Science 256:780-783(1992).
 RN [25]
 Query Match 77.6%; Score 45; DB 1; Length 770;
 Best Local Similarly 70.0%; Pred. No. 2.2;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 Oy 1 SMITNRYEDV 10
 Db 302 AMSRWTFDV 311
 RESULT 5
 A4_MOUSE
 ID A4_MOUSE STANDARD; PRT; 770 AA.
 AC P12023;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN HOMOLOGY PRECURSOR
 DE (AMYLOIDGENIC GLYCOPROTEIN) (AG).
 GN APP.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE OF 1-289 AND 365-770 FROM N.A.
 RC STRAIN=BALE/C; TISSUE=Brain;
 RX MEDLINE-92096458; Pubmed-1756177;
 RA de Strooper B., van Leeuwen F., van den Berghe H.;
 RT "The amyloid beta protein precursor or proteinase nexin II from mouse
 RT is closer related to its human homolog than previously reported.";
 RL Biochim. Biophys. Acta 1129:141-143(1991).
 RN [2]
 RP SEQUENCE OF 1-289 AND 365-770 FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE-88106489; Pubmed-3322280;
 RA Yamada T., Sasaki H., Furuya H., Miyata T., Goto I., Sakaki Y.;
 RT "Complementary DNA for the mouse homolog of the human amyloid beta
 RT protein precursor.";
 RL Biochem. Biophys. Res. Commun. 149:665-671(1987).
 RN [3]
 RP REVISIONS.
 RA Yamada T.;
 RL Submitted (MAR-1988) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE OF 289-364 FROM N.A.
 RC STRAIN=CD-1; TISSUE=Placenta;
 RX MEDLINE-89345111; Pubmed-2569710;
 RA Fukuchi K., Martin G.M., Deeb S.S.;
 RT "Sequence of the protease inhibitor domain of the A4 amyloid protein
 RT precursor of Mus domesticus.";
 RL Nucleic Acids Res. 17:5396-5396(1989).
 RN [5]
 RP SEQUENCE OF 1-19 FROM N.A.
 RX MEDLINE-92209998; Pubmed-1555768;
 RA Izumi R., Yamada T., Yoshikai S.I., Sasaki H., Hattori M.,
 RA Sakai Y.;
 RT "Positive and negative regulatory elements for the expression of the
 RT Alzheimer's disease amyloid precursor-encoding gene in mouse.";
 RL Gene 112:189-195(1992).
 RN [6]
 RP SEQUENCE OF 281-380 FROM N.A., AND ALTERNATIVE SPLICING.
 RC TISSUE=Brain, and Kidney;
 RX MEDLINE-89149813; Pubmed-2493250;
 RA Yamada T., Sasaki H., Dohura K., Goto I., Sakaki Y.;
 RT "Structure and expression of the alternatively-spliced forms of mRNA
 RT for the mouse homolog of Alzheimer's disease amyloid beta protein
 RT precursor.";

```

RL Biochem. Biophys. Res. Commun. 158:906-912(1989).
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- ALTERNATIVE PRODUCTS: 5 ISOFORMS: APP(395), APP(563), APP(695),
CC APP(751) AND APP(770) (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE
CC SPLICING.
CC -1- TISSUE SPECIFICITY: AAA(770) IS EXPRESSED IN KIDNEY. AAA(751) IS
CC WIDELY EXPRESSED. AAA(695) IS EXPRESSED IN BRAIN, KIDNEY AND
CC LIVER.
CC -1- DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL FOR ITS ASSOCIATION
CC WITH X11-ALPHA, -BETA, AND -GAMMA. THE SEQUENCE SPECIFIC
CC RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL TO THE
CC NPXY MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF
CC PHOSPHORYLATION (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -1- SIMILARITY: CONTAINS 1 BPTI/KUNITZ INHIBITOR DOMAIN.
CC -----
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CC -----
CC EMBL: X59379; -; NOT_ANNOTATED_CDS.
CC DR EMBL: M18373; AAA37139.1; -
CC DR EMBL: X15210; CAA33280.1; -
CC DR EMBL: D10603; BAA01456.1; -
CC DR EMBL: M24397; AAA3929.1; -
CC DR PIR: A27485; A27485.
CC DR PIR: S04855; S04855.
CC DR PIR: S19727; S19727.
CC DR MGI: 88059; APP.
CC DR InterPro: IPR001868; A4_APP.
CC DR InterPro: IPR002223; Kunitz_BPTI.
CC DR Pfam: PF02177; A4_EXTRA; 1.
CC DR Pfam: PF00014; Kunitz_BPTI; 1.
CC DR PRINTS: PR00203; AMYLOIDA4.
CC DR PRINTS: PR00204; BETAMYLOID.
CC DR PRINTS: S00006; BASICPTASE.
CC DR SMART: SM00006; A4_EXTRA; 1.
CC DR SMART: SM00131; KU; 1.
CC DR PROSITE: PS00319; A4_EXTRA; 1.
CC DR PROSITE: PS00320; A4_INTRA; 1.
CC DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
CC DR PROSITE: PS50279; BPTI_KUNITZ_2; 1.
CC KW Glycoprotein; Amyloid; Neurone; Transmembrane; Signal;
CC KW Alternative splicing; Serine protease inhibitor.
CC FT SIGNAL 1 770
CC FT CHAIN 18 770
CC FT DOMAIN 18 699
CC FT TRANSMEM 700 723
CC FT DOMAIN 724 770
CC FT DOMAIN 673 715
CC FT DOMAIN 287 345
CC FT SITE 759 762
CC FT DISULFID 291 341
CC FT DISULFID 300 324
CC FT DISULFID 316 337
CC FT CARBOHYD 542 542
CC FT CARBOHYD 571 571
CC FT CARBSPLIC 289 289
CC FT VARSPLIC 290 364
CC FT VARSPLIC 346 380
CC FT VARSPLIC 380 380
CC FT SEQUENCE 770 AA; 86752 MW; 26C50DE0890CA7A CRC64;

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Query Match 77.6%; Score 45; DB 1; Length 770;
Best Local Similarity 70.0%; Pred. No. 2.2;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 SMITNMYFDV 10

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DB 302 AMISRWYFDV 311
:|||||
RESULT 6
ID A4_RAT STANDARD: PRT: 770 AA.
AC P08592;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN HOMOLOG PRECURSOR
DE (AMYLOIDOGENIC GLYCOPROTEIN) (AG).
GN APP.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE OF 1-289 AND 365-770 FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=88312583; PubMed=2900758;
RA Shivers B.D., Hillich C., Malthaup G., Salbaum J.M., Beyreuther K.,
RA Seeburg P.H.;
RT "Alzheimer's disease amyloidogenic glycoprotein: expression pattern
RT in rat brain suggests a role in cell contact.";
RL EMBO J. 7:1365-1370(1988).
RN [2]
RP SEQUENCE OF 289-364 FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=89183625; PubMed=2648331;
RA Kang J., Mueller-Hill B.;
RT "The sequence of the two extra exons in rat preA4.";
RL Nucleic Acids Res. 17:2130-2130(1989).
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- ALTERNATIVE PRODUCTS: 5 ISOFORMS: APP(395), APP(563), APP(695),
CC APP(751) AND APP(770) (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE
CC SPLICING.
CC -1- DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL FOR ITS ASSOCIATION
CC WITH X11-ALPHA, -BETA, AND -GAMMA. THE SEQUENCE SPECIFIC
CC RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL TO THE
CC NPXY MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF
CC PHOSPHORYLATION (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -1- SIMILARITY: CONTAINS 1 BPTI/KUNITZ INHIBITOR DOMAIN.
CC -----
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CC -----
CC EMBL: X07648; CAA30488.1; -
CC EMBL: X14066; CAA32229.1; -
CC DR PIR: S00550; S00550.
CC DR PIR: S03607; S03607.
CC DR InterPro: IPR001868; A4_APP.
CC DR InterPro: IPR002223; Kunitz_BPTI.
CC DR Pfam: PF02177; A4_EXTRA; 1.
CC DR Pfam: PF00014; Kunitz_BPTI; 1.
CC DR PRINTS: PR00203; AMYLOIDA4.
CC DR PRINTS: PR00204; BETAMYLOID.
CC DR PRINTS: PR00759; BASICPTASE.
CC DR SMART: SM00006; A4_EXTRA; 1.
CC DR SMART: SM00006; A4_EXTRA; 1.
CC DR PROSITE: PS00319; A4_EXTRA; 1.
CC DR PROSITE: PS00320; A4_INTRA; 1.
CC DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
CC DR PROSITE: PS50279; BPTI_KUNITZ_2; 1.
CC KW Glycoprotein; Amyloid; Neurone; Transmembrane; Signal;
CC KW Alternative splicing; Serine protease inhibitor.

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FT SIGNAL 1 17 BY SIMILARITY.
FT CHAIN 18 770 ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN
FT TRANSNM 18 699 HOMOLOG.
FT DOMAIN 700 723 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 724 770 POTENTIAL.
FT DOMAIN 673 715 CYTOPLASMIC (POTENTIAL).
FT SITE 759 762 EQUIVALENT OF BETA-AMYLOID PROTEIN.
FT DISULFD 291 341 BPPI/KUNITZ INHIBITOR.
FT DISULFD 300 324 CLATHRIN-BINDING (BY SIMILARITY).
FT DISULFD 316 337 BY SIMILARITY.
FT CARBOHD 542 542 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD 571 571 E -> V (IN ISOFORM APP(695)).
FT VARSPLC 289 289 MISSING (IN ISOFORM APP(695)).
FT VARSPLC 290 364
SQ SEQUENCE 770 AA: 86704 MW: C26C9D6B2D929A7 CRC64:

Query Match 77.6%; Score 45; DB 1; Length 770;
Best Local Similarity 70.0%; Pred. No. 2.2;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 SMITNMYEDV 10
Db 302 AMISRWYFDV 311

RESULT 7
CLIP_HUMAN STANDARD: PRT: 266 AA.
ID P46060; Q15409;
AC 01-FEB-1996 (Rel. 33, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE GLIOMA PATHOGENESIS-RELATED PROTEIN (RTVP-1 PROTEIN).
GN GLIPR OR RTVP1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N. A.
RC TISSUE=Glial tumor;
RX MEDLINE=9712816; PubMed=8973356;
RA Rich T., Chen P., Furman F., Huynh N., Israel M.A.;
RT "RTVP-1, a novel human gene with sequence similarity to genes of
RT diverse species, is expressed in tumor cell lines of glial but not
RT neuronal origin.";
RL Gene 180:125-130(1996).
RN [2]
RP SEQUENCE OF 11-266 FROM N. A.
RX MEDLINE=95331646; PubMed=7607567;
RA Murphy E.V., Zhang Y., Zhu W., Biggs J.;
RT "The human glioma pathogenesis-related protein is structurally
RT related to plant pathogenesis-related proteins and its gene is
RT expressed specifically in brain tumors.";
RL Gene 159:131-135(1995).
RN [3]
RP STRUCTURE BY NMR.
RX MEDLINE=96151500; PubMed=9482873;
RA Szyperski T., Fernandez C., Wüthrich K.;
RT "Structure comparison of human glioma pathogenesis-related protein
RT GLIPR and the plant pathogenesis-related protein P1a indicates a
RT functional link between the human immune system and a plant defense
RT system.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:2262-2266(1998).
CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN THE HUMAN BRAIN TUMOR,
CC GLOBULASTOMA MULTIFORM/ASTROCYTOMA, BUT NEITHER IN NORMAL FETAL
CC OR ADULT BRAIN TISSUE, NOR IN OTHER NERVOUS SYSTEM TUMORS.
CC -1- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;
CC INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.
CC -----

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CC or send an email to license@sdb-sdb.ch).
CC -----
DR EMBL: X91911; CA63005.1; -
DR EMBL: U16307; AAA82731.1; -
DR HSSP: P04284; ICPE.
DR MIM: 602692; -
DR InterPro: IPR01283; SCP.
DR Pfam: PF00186; SCP; 1.
DR PRINTS: PR00837; V57PXLKE.
DR SMART: SM00198; SCP; 1.
DR PROSITE: PS01009; SCP_AG5_PRL_SC7_1; 1.
DR PROSITE: PS01010; SCP_AG5_PRL_SC7_2; 1.
FT CONFLICT 125 125 D -> N (IN REF. 2).
FT CONFLICT 209 266 RORDVKKRYGVVPGWFIYRNRRTSLFLVNSVILLV
FT TITLVQLKYNLVLD -> DSETKSNVTMLYIRLAHIS
FT T (IN REF. 2).
SQ SEQUENCE 266 AA: 30342 MW: C04378085EFB2B7A CRC64:

Query Match 65.5%; Score 38; DB 1; Length 266;
Best Local Similarity 60.0%; Pred. No. 12;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 SMITNMYEDV 10
Db 112 SAITNMYDEI 121

RESULT 8
ABGT_ECOLI STANDARD: PRT: 510 AA.
ID P46133; P76051; P76845; P76843;
AC 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE AMINOENZOYL-GLUTAMATE TRANSPORT PROTEIN.
GN ABGT OR B1336.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N. A., AND CHARACTERIZATION.
RC STRAIN=BN1001, AND BN1003;
RX MEDLINE=99047572; PubMed=9829935;
RA Hussein M.J., Green J.M., Nichols B.P.;
RT "Characterization of mutations that allow p-aminobenzoyl-L-glutamate
RT utilization by Escherichia coli.";
RL J. Bacteriol. 180:6260-6268(1998).
RN [2]
RP SEQUENCE FROM N. A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Borna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [3]
RP SEQUENCE FROM N. A.
RC STRAIN=K12;
RX MEDLINE=97251357; PubMed=9097039;
RA Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Itoh T.,
RA Kasai H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M.,
RA Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,
RA Nakade S., Nakamura Y., Nishimoto H., Nishio Y., Oshima T., Saito N.,

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RA Sempel G., Seki Y., Sivasundaram S., Tagami H., Takeda J.,
 RA Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T.,
 RT "A 570-kb DNA sequence of the *Escherichia coli* K-12 genome
 RT corresponding to the 28.0-40.1 min region on the linkage map.",
 RL DNA Res. 3:363-377(1996).
 RN
 RP
 RP SEQUENCE OF 454-510 FROM N.A.
 RX MEDLINE-88067749; PubMed-2825131;
 RA Potter P.M., Wilkinson M.C., Filton J., Carr F.J., Brennan J.,
 RA Cooper D.P., Margison G.P.,
 RT "Characterisation and nucleotide sequence of *ogt*, the
 RT 06-alkylguanine-DNA-alkyltransferase gene of *E. coli*.",
 RL Nucleic Acids Res. 15:9177-9193(1987).
 RN
 RP IDENTIFICATION.
 RX MEDLINE-96032851; PubMed-7567469;
 RA Borodovsky M., McIninch J., Koonin E.V., Rudd K.E., Médigue C.,
 RA Danchin A.,
 RT "Detection of new genes in a bacterial genome using Markov models for
 RT three gene classes.",
 RL Nucleic Acids Res. 23:3554-3562(1995).
 CC
 CC -1- FUNCTION: ESSENTIAL FOR AMINOENZOYL-GLUTAMATE INTO THE CELL. SEEMS ALSO TO
 CC TRANSPORT AMINOENZOYL-GLUTAMATE INTO THE CELL.
 CC INCREASE THE SENSITIVITY TO LOW LEVELS OF AMINOENZOYL-GLUTAMATE.
 CC -1- SUFFICIENT TO CONFER AMINOENZOYL-GLUTAMATE UTILIZATION PHENOTYPE.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (PROBABLY).
 CC MISCELLANEOUS: IT IS SUGGESTED THAT IN WILD-TYPE STRAIN ABGT WOULD
 CC NORMALLY BE CRYPTIC OR NOT EXPRESSED UNDER CONDITIONS OF GROWTH ON
 CC MINIMAL MEDIUM. ALTERING THE EXPRESSION OF ABGT FROM ITS WILD-TYPE
 CC CONTEXT APPEARS TO BE THE MECHANISM FOR OBTAINING THE GROWTH
 CC PHENOTYPE.
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 CC -----
 DR EMBL: AE000231; AAC74418.1; -;
 DR EMBL: D90772; BAA14939.1; ALT_INIT.
 DR EMBL: D90771; BAA14929.1; -;
 DR EcGene: Y00495; -; NOT_ANNOTATED.CDS.
 KM Transmembrane; Transport; Amino-acid transport; Complete proteome.
 FT TRANSMEM 32 52 POTENTIAL.
 FT TRANSMEM 64 84 POTENTIAL.
 FT TRANSMEM 87 107 POTENTIAL.
 FT TRANSMEM 141 161 POTENTIAL.
 FT TRANSMEM 167 187 POTENTIAL.
 FT TRANSMEM 213 233 POTENTIAL.
 FT TRANSMEM 263 283 POTENTIAL.
 FT TRANSMEM 305 325 POTENTIAL.
 FT TRANSMEM 345 365 POTENTIAL.
 FT TRANSMEM 384 404 POTENTIAL.
 FT TRANSMEM 407 427 POTENTIAL.
 FT TRANSMEM 441 461 POTENTIAL.
 FT TRANSMEM 481 501 POTENTIAL.
 FT TRANSMEM 506 506 POTENTIAL.
 FT CONFLICT 506 506 Y -> S (IN REF. 3).
 SQ SEQUENCE 510 AA; 55114 MW; C33CBCEB634B2CFC CRC64;

Query Match 65.5%; Score 38; DB 1; Length 510;
 Best Local Similarity 75.0%; Pred. No. 22;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 SMITNWF 8
 I:| | | | |
 Db 211 SVIDNWF 218

RESULT 9

SAR1_TRIE
 ID SAR1_TRIE STANDARD; PRT; 189 AA.
 AC P78976;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE GTP-BINDING PROTEIN SAR1.
 OS SAR1.
 OS Trichoderma reesei (Hypocrea jecorina).
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Hypocreales; Hypocreaceae; Hypocrea.
 ON NCBI_TaxID=51453;
 RN
 RP
 RP SEQUENCE FROM N.A.
 RC STRAIN-QM9414 / RUP C-30;
 RX MEDLINE-98055160; PubMed-9393442;
 RA Valdhuisen G., Saloheimo M., Fiers M.A., Punt P.J., Contreas R.,
 RA Penttilä M., van den Hondel C.A.,
 RT "Isolation and analysis of functional homologues of the secretion-
 RT related SAR1 gene of *Saccharomyces cerevisiae* from *Aspergillus niger*
 RT and *Trichoderma reesei*.",
 RL Mol. Gen. Genet. 256:446-455(1997).
 CC
 CC -1- FUNCTION: INVOLVED IN TRANSPORT FROM THE ENDOPLASMIC RETICULUM
 CC TO THE GOLGI APPARATUS (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE SMALL GTPASE SUPERFAMILY. SAR1 FAMILY.
 CC
 CC -----
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 CC
 CC -----
 DR EMBL: Y08636; CAA69926.1; -;
 DR InterPro: IPR000251; ARF.
 DR InterPro: IPR001806; Ras_trnsfmg.
 DR InterPro: IPR002046; Sar1_GTPBP.
 DR Pfam: PF00025; arf; 1.
 DR PRINTS: PR00328; SAR1GTPBP.
 DR PRINTS: PR00449; RASTRNSFRMG.
 DR SMART: SM00178; SAR; 1.
 DR PROSITE: PS01020; SAR1; 1.
 KM GTP-binding; Protein transport; Endoplasmic reticulum; Golgi stack.
 FT NP_BIND 27 34 GTP (BY SIMILARITY).
 FT NP_BIND 70 73 GTP (BY SIMILARITY).
 FT NP_BIND 129 132 GTP (BY SIMILARITY).
 SQ SEQUENCE 189 AA; 21546 MW; 559572F920415344 CRC64;

Query Match 63.8%; Score 37; DB 1; Length 189;
 Best Local Similarity 62.5%; Pred. No. 12;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 3 ITNNYFDV 10
 I:| | | | |
 Db 3 IYNNFYDV 10

RESULT 10
 AMYR_BACS8
 ID AMYR_BACS8 STANDARD; PRT; 713 AA.
 AC P17692;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE RAW-STARCH-DIGESTING AMYLASE PRECURSOR (EC 3.2.1.1) (1,4-ALPHA-D-
 DE GLUCAN GLUCANOHYDROLASE).
 OS Bacillus sp. (strain B1018).
 OC Bacteria; Firmicutes; Bacillus/Clostridium group;
 OC Bacillus/Staphylococcus group; Bacillus.
 ON NCBI_TaxID=1417;
 RN [1]

```

RP SEQUENCE FROM N.A., AND SEQUENCE OF 28-47.
RA MEDLINE-90147765; PubMed-1689153;
RX Itokor P., Tsukagoshi N., Udaoka S.;
RT "Nucleotide sequence of the raw-starch-digesting amylase gene from
RT Bacillus sp. B1018 and its strong homology to the cyclodextrin
RT glucanotransferase genes";
RL Biochem. Biophys. Res. Commun. 166:630-636(1990).
CC -1- FUNCTION: THIS ENDO-TYPE ADSORBABLE AMYLASE IS CAPABLE TO
CC DIGEST RAW-STARCH.
CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-ALPHA-GLUCOSIDIC
CC LINKAGES IN OLIGOSACCHARIDES AND POLYSACCHARIDES.
CC -1- COFACTOR: BINDS A CALCIUM ION REQUIRED FOR ITS ACTIVITY.
CC -1- SUBCELLULAR LOCATION: SECRETED.
CC -1- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
CC KNOWN AS THE ALPHA-AMYLASE FAMILY.
CC -----
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CC -----
DR EMBL: M33302; AAA22239.1; -
DR EMBL: D90112; BAA14140.1; -
DR PIR: A34648; A34648.
DR PIR: S09196; S09196.
DR HSSP: P43379; ICXF.
DR InterPro: IPR000461; Alpha_amylase.
DR InterPro: IPR002044; CBD_4.
DR InterPro: IPR002909; IPT_TTG.
DR Pfam: PF00128; alpha-amylase; 1.
DR Pfam: PF00686; CBD_4; 1.
DR Pfam: PF01833; TIG; 1.
DR ProDom: PD001568; CBD_4; 1.
DR HydroLase; Glycosidase; Carbohydrate metabolism; Calcium; Signal.
FT SIGNAL 1 27
FT CHAIN 28 713 RAW-STARCH-DIGESTING AMYLASE.
FT ACT_SITE 256 256 BY SIMILARITY.
FT ACT_SITE 260 260 BY SIMILARITY.
FT ACT_SITE 355 355 BY SIMILARITY.
FT ACT_SITE 713 AA: 77420 MW: 85FRB616DA687888 CRC64;
SQ SEQUENCE 713 AA: 77420 MW: 85FRB616DA687888 CRC64;

Query Match 63.8%; Score 37; DB 1; Length 713;
Best Local Similarity 83.3%; Pred. No. 47;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 NWYFDV 10
   11:11
Db 662 NWYDVF 667

RESULT 11
ID CDGU_BACCI STANDARD; PRT; 713 AA.
AC P43379;
DT 01-NOV-1995 (Rel. 32; Created)
DT 01-NOV-1995 (Rel. 32; Last sequence update)
DT 15-JUL-1999 (Rel. 38; Last annotation update)
DE CYCLOMALTODEXTRIN GLUCANOTRANSFERASE PRECURSOR (EC 2.4.1.19)
DE (CYCLODEXTRIN-GLYCOSYLTRANSFERASE) (CGTASE).
OS Bacillus circulans.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
OX NCBI_TaxID=1397;
RN [1]
RP SEQUENCE FROM N.A., AND X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
RC STRAIN=251;
RA MEDLINE-94149761; PubMed-8107143;
RA Lawson C.L., van Montfort R., Strokopytov B., Rozedoom H.J.,
RA Kalk K.H., de Vries G.E., Penninga D., Dijkhuizen L., Dijkstra B.W.;

```

```

RT "Nucleotide sequence and X-ray structure of cyclodextrin
RT glycosyltransferase from Bacillus circulans strain 251 in a maltose-
RT dependent crystal form.";
RL J. Mol. Biol. 236:590-600(1994).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).
RC STRAIN=251;
RA MEDLINE-96094317; PubMed-7493956;
RA Knegetel R.M.A., Strokopytov B., Penninga D., Faber O.G.,
RA Rozedoom H.J., Kalk K.H., Dijkstra B.W., Dijkhuizen L.;
RT "Crystallographic studies of the interaction of cyclodextrin
RT glycosyltransferase from Bacillus circulans strain 251 with natural
RT substrates and products.";
RL J. Biol. Chem. 270:29256-29264(1995).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
RA MEDLINE-97115811; PubMed-8955113;
RA Penninga D., van der Veen B.A., Knegetel R.M., van Hilum S.A.,
RA Rozedoom H.J., Kalk K.H., Dijkstra B.W., Dijkhuizen L.;
RT "The raw starch binding domain of cyclodextrin glycosyltransferase
RT from Bacillus circulans strain 251.";
RL J. Biol. Chem. 271:32777-32784(1996).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF COMPLEX WITH INHIBITOR.
RC STRAIN=251;
RA MEDLINE-96264806; PubMed-8672460;
RA Strokopytov B., Knegetel R.M.A., Penninga D., Rozedoom H.J., Kalk K.H.,
RA Dijkhuizen L., Dijkstra B.W.;
RT "Structure of cyclodextrin glycosyltransferase complexed with a
RT maltanose inhibitor at 2.6-A resolution. Implications for product
RT specificity 35:4241-4249(1996).
CC -1- CATALYTIC ACTIVITY: DEGRADE STARCH TO CYCLODEXTRINS BY FORMATION
CC OF A 1,4-ALPHA-D-GLUCOSIDIC BOND.
CC -1- COFACTOR: BINDS TWO CALCIUM IONS.
CC -1- SUBUNIT: MONOMER.
CC -1- DOMAIN: MAY CONSIST OF TWO PROTEIN DOMAINS. THE ONE IN THE AMINO-
CC TERMINAL SIDE CLEAVES THE ALPHA-1,4-GLUCOSIDIC BOND IN STARCH, AND
CC THE OTHER IN THE C-TERMINAL SIDE CATALYZES OTHER ACTIVITIES,
CC INCLUDING THE RECONSTITUTION OF AN ALPHA-1,4-GLUCOSIDIC LINKAGE
CC FOR CYCLIZING THE MALTOOLIGOSACCHARIDE PRODUCED.
CC -1- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
CC KNOWN AS THE ALPHA-AMYLASE FAMILY.
CC -----
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CC -----
DR EMBL: X78145; CAA55023.1; -
DR PDB: 2CXG; 14-OCT-98.
DR PDB: 1CDG; 08-MAR-95.
DR PDB: 1CGV; 27-FEB-95.
DR PDB: 1CGW; 27-FEB-95.
DR PDB: 1CGX; 07-FEB-95.
DR PDB: 1CGY; 07-FEB-95.
DR PDB: 1CXE; 15-DEC-95.
DR PDB: 1CXF; 15-DEC-95.
DR PDB: 1CXH; 15-DEC-95.
DR PDB: 1CXI; 15-DEC-95.
DR PDB: 2DIJ; 13-JAN-99.
DR PDB: 1TCM; 21-APR-97.
DR InterPro: IPR000461; Alpha_amylase.
DR InterPro: IPR002044; CBD_4.
DR InterPro: IPR002909; IPT_TTG.
DR Pfam: PF00128; alpha-amylase; 1.
DR Pfam: PF00686; CBD_4; 1.
DR Pfam: PF01833; TIG; 1.
DR ProDom: PD001568; CBD_4; 1.
DR Transferase; Glycosyltransferase; Calcium; Signal; 3D-structure.
KW

```


FT SIGNAL 1 25
 FT CHAIN 26 713 CYCLOMALPRODEXTRIN GLUCANOTRANSFERASE.
 FT DOMAIN 28 165 A1.
 FT DOMAIN 166 229 B.
 FT DOMAIN 230 433 A2.
 FT DOMAIN 434 522 C.
 FT DOMAIN 523 609 D.
 FT DOMAIN 610 713 E.
 FT DISULFID 70 77
 FT ACT_SITE 256 256 NUCLEOPHILE.
 FT ACT_SITE 284 284 PROTON DONOR.
 FT ACT_SITE 355 355 SUBSTRATE-BINDING.
 SQ SEQUENCE 713 AA; 77309 MW; 8ABBF2C633A004B CRC64;

Query Match 63.88; Score 37; DB 1; Length 713;
 Best Local Similarity 83.3%; Pred. No. 47;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 5 NWYEDV 10
 |||:|
 Db 662 NWYIDV 667

RESULT 12

RR2_PEA STANDARD; PRT; 236 AA.

AC P08241;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DT 01-FEB-1996 (Rel. 33, Last annotation update)
 DE CHLOROPLAST 30S RIBOSOMAL PROTEIN S2.
 GN RPS2.
 OS Pisum sativum (Garden pea).
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Viciae; Viciae;
 OC NCBI_Taxid=3888;
 RX MEDLINE=86323089; PubMed=3530249;
 RA Cozens A.L., Walker J.E.;
 RA "Pea chloroplast DNA encodes homologues of Escherichia coli ribosomal
 subunit S2 and the beta'-subunit of RNA polymerase.";
 RT Biochem. J. 236:453-460(1986).
 RN [2]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=86323089; PubMed=3530249;
 RA Hudson G.S., Mason J.C., Holton T.A., Koller B., Cox G.B.,
 RA Whitfield P.R., Bottomley W.;
 RA "A gene cluster in the spinach and pea chloroplast genomes encoding
 one cpl and three cfo subunits of the H⁺-ATP synthase complex and the
 ribosomal protein S2.";
 RT J. Mol. Biol. 196:283-298(1987).
 RL J. Mol. Biol. 196:283-298(1987).
 CC -1- SIMILARITY: BELONGS TO THE S2P FAMILY OF RIBOSOMAL PROTEINS.
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 CC
 CC EMBL: X03912; CA27546.1; -;
 DR EMBL: X05917; CAA29348.1; -;
 DR PIR: S08586; R3PM2.
 DR Mendel: 4173; PISA: rps2.1.
 DR InterPro: IPR001865; Ribosomal_S2.
 DR Pfam: PF00318; Ribosomal_S2; 1.
 DR PRINTS: PR00395; RIBOSOMAL_S2.
 DR PROSITE: PS00962; RIBOSOMAL_S2_1; 1.

DR PROSITE: PS00962; RIBOSOMAL_S2_2; 1.
 KW Ribosomal protein; Chloroplast.
 SQ SEQUENCE 236 AA; 26842 MW; E4C8A8B5827B4154 CRC64;

Query Match 62.1%; Score 36; DB 1; Length 236;
 Best Local Similarity 83.3%; Pred. No. 22;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 MTNMY 7
 |||||
 Db 104 MTNMY 109

RESULT 13

KMLC_RABIT STANDARD; PRT; 607 AA.

AC P07313;
 DT 01-APR-1988 (Rel. 07, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE MYOSIN LIGHT CHAIN KINASE, SKELETAL MUSCLE (EC 2.7.1.117) (MCK).
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OC NCBI_Taxid=9986;
 RX MEDLINE=90110242; PubMed=1688558;
 RA Herring B.P., Stull J.T., Gallagher P.J.;
 RA "Domain characterization of rabbit skeletal muscle myosin light chain
 kinase.";
 RT J. Biol. Chem. 265:1724-1730(1990).
 RN [2]
 RN SEQUENCE OF 1-603.
 RX MEDLINE=87101105; PubMed=3542042;
 RA Takio K., Blumenthal D.K., Walsh K.A., Titani K., Krebs E.G.;
 RA "Amino acid sequence of rabbit skeletal muscle myosin light chain
 kinase.";
 RT Biochemistry 25:8049-8057(1986).
 RN [3]
 RN SEQUENCE OF 295-603.
 RX MEDLINE=86104095; PubMed=3841288;
 RA Takio K., Blumenthal D.K., Edelman A.M., Walsh K.A., Krebs E.G.,
 RA Titani K.;
 RA "Amino acid sequence of an active fragment of rabbit skeletal muscle
 myosin light chain kinase.";
 RT Biochemistry 24:6028-6037(1985).
 RN [4]
 RN STRUCTURE BY NMR OF 577-602.
 RX MEDLINE=92263094; PubMed=1585175;
 RA Ikura M., Clore G.M., Gronenborn A.M., Zhu G., Klee C.B., Bax A.;
 RA "Solution structure of a calmodulin-target peptide complex by
 multidimensional NMR.";
 RT Science 256:632-638(1992).
 RL Science 256:632-638(1992).
 CC -1- FUNCTION: PHOSPHORYLATES A SPECIFIC SERINE IN THE N-TERMINUS OF A
 MYOSIN LIGHT CHAIN.
 CC -1- CATALYTIC ACTIVITY: ATP + [MYOSIN LIGHT-CHAIN] = ADP + [MYOSIN
 LIGHT-CHAIN] PHOSPHATE.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
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 CC
 CC EMBL: J05194; AAA31400.1; -;
 DR PIR: A25830; A25830.
 DR PIR: A05120; A05120.
 DR PIR: A35021; A35021.

```

DR PDB: 2BBM; 31-JAN-94.
DR PDB: 2BBN; 31-JAN-94.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR002290; Ser_thr_kin_actsite.
DR Pfam: PF00069; pkinase; 1.
DR SMART: SM00220; S_TKC; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
DR Transferase: Serine/threonine-protein kinase: Calmodulin-binding:
  ATP-binding; Phosphorylation; Acetylation; 3D-structure.
KW INIT_MET 0
FT MOD_RES 1 1 ACETYLATION.
FT DOMAIN 296 551 PROTEIN KINASE.
FT BINDING 585 597 CALMODULIN-BINDING.
FT NP_BIND 302 310 ATP (BY SIMILARITY).
FT BINDING 325 335 ATP (BY SIMILARITY).
FT ACT_SITE 417 417 BY SIMILARITY.
FT CONFLICT 335 335 K -> KK (IN REF. 2 AND 3).
FT HELIX 381 595
FT TURN 596 596
SQ SEQUENCE 607 AA; 65337 MW; 6E677641751A04C8 CRC64;

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Query Match      62.1%; Score 36; DB 1; Length 607;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 5 NMVFD 9
   11111
DB 509 NMVFD 513

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RESULT 14

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ID KMLC_RAT STANDARD: PRT: 609 AA.
AC P20689;
DT 01-FEB-1991 (rel. 17, Last sequence update)
DT 01-FEB-1991 (rel. 17, Last sequence update)
DT 20-AUG-2001 (rel. 40, Last annotation update)
DE MYOSIN LIGHT CHAIN KINASE, SKELETAL MUSCLE (EC 2.7.1.117) (MLCK).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxId=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88273159; PubMed=2839493;
RA Roush C.L., Kennelly P.J., Glaesum M.B., Helfman D.M., Scott J.D.,
  Krebs E.G.;
  "Isolation of the cDNA encoding rat skeletal muscle myosin light
  chain kinase. Sequence and tissue distribution.";
  J. Biol. Chem. 263:10510-10516(1988).
CC -1- FUNCTION: PHOSPHORYLATES A SPECIFIC SERINE IN THE N-TERMINUS OF A
  MYOSIN LIGHT CHAIN.
CC -1- CATALYTIC ACTIVITY: ATP + [MYOSIN LIGHT-CHAIN] - ADP + [MYOSIN
  LIGHT-CHAIN] PHOSPHATE.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC -----
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CC -----
CC EMBL: J03886; AAA41625.1; ALT_SEQ.
CC PIR: A28798; A28798.
CC HSSP: P07313; 2BBN.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR002290; Ser_thr_kin_actsite.
DR Pfam: PF00069; pkinase; 1.

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DR SMART: SM00220; S_TKC; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR Transferase: Serine/threonine-protein kinase: Calmodulin-binding:
  ATP-binding; Phosphorylation; Acetylation.
KW INIT_MET 0
FT MOD_RES 1 1 ACETYLATION (BY SIMILARITY).
FT DOMAIN 298 553 PROTEIN KINASE.
FT BINDING 587 599 CALMODULIN-BINDING (BY SIMILARITY).
FT NP_BIND 304 312 ATP (BY SIMILARITY).
FT BINDING 327 337 ATP (BY SIMILARITY).
FT ACT_SITE 419 419 BY SIMILARITY.
FT CONFLICT 337 337 K -> KK (IN REF. 2 AND 3).
SQ SEQUENCE 609 AA; 65685 MW; 0073A22659BD1358 CRC64;

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Query Match      62.1%; Score 36; DB 1; Length 609;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 5 NMVFD 9
   11111
DB 511 NMVFD 515

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RESULT 15

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ID LIR2_HUMAN STANDARD: PRT: 638 AA.
AC P53671;
DT 01-OCT-1996 (rel. 34, Created)
DT 01-OCT-1996 (rel. 34, Last sequence update)
DT 20-AUG-2001 (rel. 40, Last annotation update)
DE LIM DOMAIN KINASE 2 (EC 2.7.1.-) (LIMK-2).
GN LIMK2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96125122; PubMed=8537403;
RA Okano I., Hirooka J., Otera H., Nunoue K., Ohashi K., Iwashita S.,
  Hirai M., Mizuno K.;
  "Identification and characterization of a novel family of
  serine/threonine kinases containing two N-terminal LIM motifs.";
  J. Biol. Chem. 270:31321-31330(1995).
RN [2]
RP SEQUENCE FROM N.A.
RA Du Z., Scheet P., Harper M.;
  Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: DISPLAYS SERINE/THREONINE-SPECIFIC PHOSPHORYLATION OF
  MYELIN BASIC PROTEIN AND HISTONE (MBP) IN VITRO.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- TISSUE SPECIFICITY: HIGHEST EXPRESSION IN THE PLACENTA; MODERATE
  LEVEL IN LIVER, LUNG, KIDNEY, AND PANCREAS.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC -1- SIMILARITY: CONTAINS 2 LIM DOMAINS. THE LIM DOMAIN BINDS 2 ZINC
  IONS.
CC -----
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CC -----
CC EMBL: D45906; BAA08312.1; -.
CC HSSP: AC002073; AAB54056.1; -.
DR InterPro: IPR002290; Ser_thr_kin_actsite.
DR HMM: 601988; -.

```

DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR001781; LIM.
 DR InterPro: IPR001478; PDZ.
 DR Pfam: PF00412; LIM; 2.
 DR Pfam: PF00595; PDZ; 1.
 DR Pfam: PF00069; pkinase; 1.
 DR PRODOM: PD000094; LIM; 2.
 DR SMART: SM00132; LIM; 2.
 DR SMART: SM00228; PDZ; 1.
 DR SMART: SM00221; STYKc; 1.
 DR PROSITE: PS00478; LIM_DOMAIN_1; 2.
 DR PROSITE: PS50023; LIM_DOMAIN_2; 2.
 DR PROSITE: PS50106; PDZ; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_SF; FALSE_NEG.
 KW transferase; Serine/threonine-protein kinase; ATP-binding; Repeat;
 KW LIM domain; Metal-binding; Zinc.
 FT DOMAIN 12 63 LIM 1.
 FT DOMAIN 72 124 LIM 2.
 FT DOMAIN 152 239 PDZ.
 FT NP_BIND 331 608 PROTEIN_KINASE.
 FT NP_BIND 337 345 ATP (BY SIMILARITY).
 FT BINDING 360 360 ATP (BY SIMILARITY).
 FT ACT_SITE 451 451 BY SIMILARITY.
 SQ SEQUENCE 638 AA; 72232 MW; FB51813D99AFAC18 CRC64;

Query Match 62.1%; Score 36; DB 1; Length 638;
 Best Local Similarity 57.1%; Pred. No. 61;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 ITNMYFD 9
 DB 47 LTNMYTE 53

Search completed: February 20, 2002, 12:17:07
 Job time: 118 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 20, 2002, 12:15:09 ; Search time 12.81 Seconds

(without alignments)
59.465 Million cell updates/sec

Title: US-09-724-396-3
Perfect score: 58
Sequence: 1 SMITNMYFDV 10

Scoring table: BL0SUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Query length	DB ID	Description
1	45	77.6	76	2	S04855 Alzheimer's disease
2	45	77.6	76	2	S03607 Alzheimer's disease
3	45	77.6	76	2	S06678 Alzheimer's disease
4	45	77.6	100	2	A32282 Alzheimer's disease
5	45	77.6	484	4	A32761 hypothetical Alzhe
6	45	77.6	770	1	ORH04 Alzheimer's disease
7	42	72.4	747	2	JH0773 Alzheimer's disease
8	41	70.7	123	2	PT0383 Ig heavy chain V r
9	41	70.7	123	2	PT0385 Ig heavy chain V r
10	40	69.0	111	2	PH1019 Ig heavy chain V r
11	40	69.0	118	2	A32530 Ig heavy chain V r
12	40	69.0	123	2	PT0387 Ig heavy chain V r
13	40	69.0	123	2	PT0386 Ig heavy chain V r
14	39	67.2	474	2	A71533 probable phosphoi
15	39	67.2	474	2	H81688 phospholipase D fa
16	38	65.5	194	2	T19301 hypothetical prote
17	38	65.5	219	2	JC4131 glioma pathogene
18	38	65.5	237	2	JC5309 testis-specific, v
19	38	65.5	265	2	A85750 hypothetical prote
20	38	65.5	266	2	JC5308 testis-specific, v
21	38	65.5	510	2	C64883 membrane protein y
22	37	63.8	110	2	PH1652 Ig heavy chain V r
23	37	63.8	383	2	PT0593 glycosyltransferas
24	37	63.8	416	2	T45051 hypothetical prote
25	37	63.8	431	2	T18753 hypothetical prote
26	37	63.8	713	2	S09196 cyclomaltodextrin
27	37	63.8	713	2	A58800 cyclomaltodextrin
28	37	63.8	848	2	T34823 probable turgor pr
29	37	63.8	5126	2	S40450 ryanodine receptor

30	36	62.1	64	2	B36025 Ig heavy chain V r
31	36	62.1	122	2	PH0887 Ig heavy chain V r
32	36	62.1	123	2	PT0354 Ig heavy chain V r
33	36	62.1	125	2	C30540 Ig heavy chain V r
34	36	62.1	236	1	R3PM2 ribosomal protein
35	36	62.1	350	2	I78848 LIM-2c - rat
36	36	62.1	551	2	T26079 hypothetical prote
37	36	62.1	608	2	A35021 myosin-light-chain
38	36	62.1	610	2	A28798 myosin-light-chain
39	36	62.1	617	1	T17251 LIM motif-contain
40	36	62.1	617	1	I78847 LIM motif-contain
41	36	62.1	617	2	JC5814 LIM motif-contain
42	36	62.1	638	1	A59196 LIM motif-contain
43	36	62.1	638	1	I78846 LIM motif-contain
44	36	62.1	638	2	JC5813 LIM motif-contain
45	36	62.1	642	1	JP0079 LIM protein kinase

ALIGNMENTS

RESULT 1
S04855 Alzheimer's disease amyloid A4 protein - mouse (fragment)
C:Species: Mus musculus domesticus (western European house mouse)
C:Date: 28-Feb-1990 #sequence=revision 28-Feb-1990 #text_change 13-Aug-1999
C:Accession: S04855
R:Fukuchi, K.I.; Martin, G.M.; Deeb, S.S.
Nucleic Acids Res. 17, 5386, 1989
A:Title: Sequence of the protease inhibitor domain of the A4 amyloid protein precursor
A:Reference number: S04855; MUID:89345111
A:Accession: S04855
A:Molecule type: mRNA
A:Residues: 1-76 <RNA>
A:Cross-references: EMBL:X15210; NID:g49965; PIDN:CA33280.1; PID:g930133
A:Note: The authors translated the codon GAT for residue 74 as Val
C:Superfamily: Alzheimer's disease amyloid beta protein; animal kunitz-type protein
C:Keywords: alternative splicing; serine proteinase inhibitor; transmembrane protein
F.3-53/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 77.6%; Score 45; DB 2; Length 76;
Best Local Similarity 70.0%; Pred. No. 0.34;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 SMITNMYFDV 10
DB 14 AMISRWYFDV 23

RESULT 2
S03607 Alzheimer's disease amyloid A4 protein - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 07-Sep-1990 #sequence=revision 07-Sep-1990 #text_change 13-Aug-1999
C:Accession: S03607
R:Kang, J.; Mueller-Hill, B.
Nucleic Acids Res. 17, 2130, 1989
A:Title: The sequence of the two extra exons in rat preA4.
A:Reference number: S03607; MUID:89183625
A:Accession: S03607
A:Molecule type: mRNA
A:Residues: 1-76 <RNA>
A:Cross-references: F.3-53/X14066; NID:g56957; PIDN:CA332229.1; PID:g930262
C:Superfamily: Alzheimer's disease amyloid beta protein; animal kunitz-type protein
C:Keywords: alternative splicing; serine proteinase inhibitor; transmembrane protein
F.3-53/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 77.6%; Score 45; DB 2; Length 76;
Best Local Similarity 70.0%; Pred. No. 0.34;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 SMITNMYFDV 10
:||:|||||
Db 14 AMISRMVFDV 23

RESULT 3

s06678

Alzheimer's disease amyloid beta protein - rhesus macaque (fragment)

C:Species: Macaca mulatta (rhesus macaque)

C:Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 13-Aug-1999

C:Accession: S06678

R:Koo, E.H.; Sisodia, S.S.; Price, D.L.

submitted to the EMBL Data Library, July 1989

A:Reference number: S06678

A:Accession: S06678

A:Molecule type: mRNA

A:Residues: 1-76 <KOO>

A:Cross-references: EMBL:X15985; NID:q38080; PIDN:CAA34116.1; PID:q930135

C:Superfamily: Alzheimer's disease amyloid beta protein; animal kunitz-type proteinase

C:Keywords: alternative splicing; serine proteinase inhibitor

F:3-53/Domain: animal kunitz-type proteinase inhibitor homology <BPI>

Query Match 77.6%; Score 45; DB 2; Length 76;
Best Local Similarity 70.0%; Pred. No. 0.34;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 SMITNMYFDV 10
:||:|||||
Db 14 AMISRMVFDV 23

RESULT 4

A32282

Alzheimer's disease amyloid beta protein precursor - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 17-Aug-1989 #sequence_revision 17-Aug-1989 #text_change 13-Aug-1999

C:Accession: A32282

R:Yamada, T.; Sasaki, H.; Dohura, K.; Goto, I.; Sasaki, Y.

Biochem. Biophys. Res. Commun. 158, 906-912, 1989

A:Title: Structure and expression of the alternatively-spliced forms of mRNA for the mouse

A:Reference number: A32282; MUID:89149813

A:Accession: A32282

A:Molecule type: mRNA

A:Status: preliminary

A:Residues: 1-100 <YAM>

A:Cross-references: GB:M24397; NID:q200350; PIDN:AAA39929.1; PID:q200351

C:Superfamily: Alzheimer's disease amyloid beta protein; animal kunitz-type proteinase

C:Keywords: alternative splicing

F:11-61/Domain: animal kunitz-type proteinase inhibitor homology <BPI>

Query Match 77.6%; Score 45; DB 2; Length 100;
Best Local Similarity 70.0%; Pred. No. 0.45;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 SMITNMYFDV 10
:||:|||||
Db 22 AMISRMVFDV 31

RESULT 5

A32761

hypothetical Alzheimer's disease amyloid beta protein, Alu-containing clone - human (fr

C:Species: Homo sapiens (man)

C:Date: 29-Jan-1990 #sequence_revision 10-Apr-1996 #text_change 10-Apr-1996

C:Accession: A32761

R:de Sauvage, F.; Octave, J. N.

Science 245, 651-653, 1989

A:Title: A novel mRNA of the A4 amyloid precursor gene coding for a possibly secreted pr

A:Reference number: A32761; MUID:89346754

A:Accession: A32761

A:Molecule type: mRNA

A:Residues: 1-484 <DES>
A:Cross-references: GB:M28373
A:Note: the authors translated the codon ATG for residue 433 as Leu
C:Comment: This is the hypothetical translation of a sequence believed to contain clo
C:Keywords: cloning artifact

Query Match 77.6%; Score 45; DB 4; Length 484;
Best Local Similarity 70.0%; Pred. No. 2.4;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 SMITNMYFDV 10
:||:|||||
Db 223 AMISRMVFDV 232

RESULT 6

ORHUA4

Alzheimer's disease amyloid beta protein precursor [validated] - human

N:Alternate names: Alzheimer's disease amyloid A4 protein; coagulation factor X1a inh

N:Contains: amyloid beta protein long, plaque form; amyloid beta protein short, vascu

protein precursor splice form APP(770)

C:Species: Homo sapiens (man)

C:Date: 30-Jun-1987 #sequence_revision 28-Jul-1995 #text_change 15-Sep-2000

C:Accession: S02260; S05194; A32277; A33260; A35486; I39452; I39451; I39453; I59562;

4688; A28583; A29302; A60805; J10038; S06121; A60355; A59011; A38384; S29076; S38252;

R:Lemaire, H.G.; Salbaum, J.M.; Mulhaup, G.; Kang, J.; Bayney, R.M.; Unterbeck, A.;

Nucleic Acids Res. 17, 517-522, 1989

A:Title: The PreA4(695) precursor protein of Alzheimer's disease A4 amyloid is encode

A:Reference number: S02260; MUID:89128427

A:Accession: S02260

A:Molecule type: DNA

A:Residues: 1-288, 'V', 365-770 <LEM1>

A:Cross-references: EMBL:X13466

A:Note: alternative splice form APP(695)

R:Lemaire, H.G.

submitted to the EMBL Data Library, November 1988

A:Reference number: S05194

A:Accession: S05194

A:Molecule type: DNA

A:Residues: 1-14, 'W', 17-288, 'V', 365-770 <LEM2>

A:Cross-references: EMBL:X13466; NID:q35598; PIDN:CAA31830.1; PID:g871360

A:Note: alternative splice form APP(695)

A:Accession: A33277

A:Molecule type: DNA

A:Residues: 1-75 <LAF>

A:Cross-references: GB:M24546; GB:M24547; NID:q341202; PIDN:AAC13654.1; PID:g516074

R:Johnstone, E.M.; Chaney, M.O.; Moore, R.E.; Ward, K.E.; Norris, F.H.; Little, S.P.

Biochem. Biophys. Res. Commun. 163, 1248-1255, 1989

A:Title: Alzheimer's disease amyloid peptide is encoded by two exons and shows simila

A:Reference number: A33260; MUID:89392030

A:Accession: A33260

A:Molecule type: DNA

A:Residues: 656-737 <JOH>

A:Cross-references: GB:M29270; NID:q178863; PIDN:AAA51768.1; PID:g178865

R:Prelli, F.; Levy, E.; Van Duijn, S.G.; Bots, G.T.A.M.; Luyendijk, W.; Frangione, B

Biochem. Biophys. Res. Commun. 170, 301-307, 1990

A:Title: Expression of a normal and variant Alzheimer's beta-protein gene in amyloid

A:Reference number: A35486; MUID:90321244

A:Accession: A35486

A:Molecule type: DNA

A:Residues: 672-710 <PRE1>

A:Note: 693-Gln was found in DNA isolated from HCHNA-D patients

R:Yoshikai, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sasaki, Y.

Gene 87, 257-263, 1990

A:Title: Genomic organization of the human amyloid beta-protein precursor gene.

A:Reference number: I39451; MUID:90236318

A:Accession: I39452

A:Status: nucleic acid sequence not shown; translation not shown; translated from GB/

A:Molecule type: DNA
A:Residues: 1-770 <YOS1>
A:Cross-references: GB:M33112; NID:q178613; PIDN:AA859502.1; PID:q178616
A:Accession: I39451
A>Status: nucleic acid sequence not shown; translation not shown; translated from GB/EMBL
A:Molecule type: DNA
A:Residues: 1-530, 'QMLMPVTPAEWAKVR' <YOS2>
A:Cross-references: GB:M34875; NID:q178608; PIDN:AA859501.1; PID:q178615
R:Yoshikiri, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sekeki, Y.
Gene 102, 291-292, 1991
A:Reference number: A59020; MUID:91340168
A:Accession: I39453
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 656-737 <LEV>
A:Cross-references: GB:M37896; NID:q178618; PIDN:AA51727.1; PID:q178620
A:Note: a mutation with 693-Gln is presented
R:Murrell, J.; Farlow, M.; Gheilt, B.; Benson, M.D.
Science 254, 97-99, 1991
A:Title: A mutation in the amyloid precursor protein associated with hereditary Alzheimer
A:Reference number: I59562; MUID:92022553
A:Accession: I59562
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 689-716, 'F', 718-737 <MUR>
A:Cross-references: GB:S57665; NID:q236720; PIDN:AA819991.1; PID:q236721
R:Kamino, K.; Orr, H.T.; Payami, H.; Wilsman, E.M.; Alonso, M.E.; Puls, S.M.; Anderson, A.;
Arai, S.E.; Korenberg, J.R.; Sharma, V.; Kukul, W.; Larson, E.; Heston, L.L.; Martin, J.
Hum. Genet. 51, 998-1014, 1992
A:Title: Linkage and mutational analysis of familial Alzheimer disease kindreds for the
A:Reference number: AA4017; MUID:93035397
A:Accession: AA4017
A:Molecule type: DNA
A:Residues: 687-692, 'G', 694-718 <KAM1>
A:Cross-references: GB:S45135; NID:q257377; PIDN:AA83645.1; PID:q257378
A:Experimental source: familial Alzheimer disease family S18
A:Note: sequence extracted from NCBI backbone (NCBIP:115374)
A:Accession: B44017
A:Molecule type: DNA
A:Residues: 687-718 <KAM2>
A:Cross-references: GB:S45136; NID:q257379; PIDN:AA83646.1; PID:q257380
A:Experimental source: familial Alzheimer disease family L1
A:Note: sequence extracted from NCBI backbone (NCBIP:115376)
R:Kang, J.; Lemaire, H.G.; Unterbeck, A.; Salbaum, J.M.; Masters, C.L.; Grzeschik, K.H.;
Nature 325, 733-736, 1987
A:Title: The precursor of Alzheimer's disease amyloid A4 protein resembles a cell-surf
A:Reference number: A03134; MUID:87144572
A:Accession: A03134
A:Molecule type: mRNA
A:Residues: 1-288, 'V', 365-770 <KAN>
A:Cross-references: GB:Y00264; NID:q28525; PIDN:CAA6374.1; PID:q28526
R:Robbitt, N.K.; Ramakrishna, N.; Wolfe, G.; Wisniewski, H.M.
Proc. Natl. Acad. Sci. U.S.A. 84, 4190-4194, 1987
A:Title: Molecular cloning and characterization of a cDNA encoding the cerebrovascular
A:Reference number: A29030; MUID:87231971
A:Accession: A29030
A:Molecule type: mRNA
A:Residues: 284-288, 'V', 365-646, 'E', 648-770 <ROB>
A:Cross-references: GB:M16765; NID:q178539; PIDN:AA51722.1; PID:q178540
A:Note: the authors translated the codon GAG for residue 647 as Asp
R:Goldgaber, D.; Lerman, M.I.; McBride, O.W.; Saffioti, U.; Gajdusek, D.C.
Science 235, 877-880, 1987
A:Title: Characterization and chromosomal localization of a cDNA encoding brain amyloid
A:Reference number: A47584; MUID:87120328
A:Accession: A47584

A:Molecule type: mRNA
A:Residues: 674-756, 'S', 758-770 <GOL>
A:Cross-references: GB:M15533; NID:q178706; PIDN:AA35540.1; PID:q178707
A:Experimental source: brain
R:Tanz, R.E.; Gusella, J.F.; Watkins, P.C.; Bruns, G.A.P.; St George-Hyslop, P.; Van
Science 235, 880-884, 1987
A:Title: Amyloid beta protein gene: cDNA, mRNA distribution, and genetic linkage near
A:Reference number: A47585; MUID:87120329
A:Accession: A47585
A:Molecule type: mRNA
A:Residues: 674-703 <TAN1>
A:Cross-references: GB:M15532; NID:q177957; PIDN:AA51564.1; PID:q177958
R:Dyck, T.; Weidemann, A.; Multhaup, G.; Salbaum, J.M.; Lemaire, H.G.; Kang, J.; Mue
EMBO J. 7, 949-957, 1988
A:Title: Identification, transmembrane orientation and biogenesis of the amyloid A4 p
A:Reference number: S02638; MUID:88266437
A:Accession: S02638
A:Molecule type: mRNA
A:Residues: 672-678 <DYP>
R:Tanz, R.E.; McClatchey, A.I.; Lampert, E.D.; Villa-Komaroff, L.; Gusella, J.F.; N
Nature 331, 528-530, 1988
A:Title: Protease inhibitor domain encoded by an amyloid protein precursor mRNA assoc
A:Reference number: S00707; MUID:88122640
A:Accession: S00707
A:Molecule type: mRNA
A:Residues: 286-344, 'I', 365-366 <TAN2>
A:Cross-references: EMBL:X06982; NID:q28817; PIDN:CAA30042.1; PID:q929612
A:Experimental source: promyelocytic leukemia cell line HL60
R:Ponte, P.; Gonzalez-Demhitt, P.; Schilling, J.; Miller, J.; Hsu, D.; Greenberg, B.;
Nature 331, 525-527, 1988
A:Title: A new A4 amyloid mRNA contains a domain homologous to serine proteinase inh
A:Reference number: S00925; MUID:88122639
A:Accession: S00925
A:Molecule type: mRNA
A:Residues: 1-344, 'I', 365-770 <PO2>
A:Cross-references: GB:X06989; EMBL:X00297; NID:q28720; PIDN:CAA30050.1; PID:q28721
A:Note: alternative splice form APP(751)
R:Kitaguchi, N.; Takahashi, Y.; Tokushima, Y.; Shiojiri, S.; Ito, H.
Nature 331, 530-532, 1988
A:Title: Novel precursor of Alzheimer's disease amyloid protein shows protease inhibi
A:Reference number: A38949; MUID:88122641
A:Accession: A38949
A:Molecule type: mRNA
A:Residues: 287-367 <KIN>
A:Cross-references: GB:X06981; NID:q28816; PIDN:CAA30041.1; PID:q929611
A:Experimental source: glioblastoma cell line
A:Note: alternative splice form APP(770)
R:Vitek, M.P.; Rasool, C.G.; de Sauvage, F.; Vitek, S.M.; Bartus, R.T.; Beer, B.; Ash
Brain Res. Mol. Brain Res. 4, 121-131, 1988
A:Title: Absence of mutation in the beta-amyloid cDNAs cloned from the brains of thre
A:Reference number: A30320
A:Accession: A30320
A>Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 284-288, 'V', 365-770 <VIT1>
A:Accession: B30320
A:Molecule type: mRNA
A:Residues: 122-288, 'V', 365-770 <VIT2>
A:Accession: C30320
A>Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 606-770 <VIT3>
R:Zain, S.B.; Salim, M.; Sajdel-Sulkowska, E.M.; Majocha, R.E.; Marotta,
Proc. Natl. Acad. Sci. U.S.A. 85, 929-933, 1988
A:Title: Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer disease
A:Reference number: A31087; MUID:88124954
A:Accession: A31087
A:Molecule type: mRNA
A:Residues: 507-770 <ZAI>
A:Cross-references: GB:M18734; NID:q178572; PIDN:AA51726.1; PID:q178573
A:Note: the authors translated the codon GAA for residue 599 as Gly, ACC for residue

8 as Val, CNG for residue 609 as Asn, AAT for residue 610 as Gly, and GGT for residue 65
 A:Note: the cited Genbank accession number, J03594, is not in release 101.0
 R:Masters, C.L.; Multhaup, G.; Simms, G.; Potgiesser, J.; Martins, R.N.; Beyreuther, K.

Query Match 77.6% Score 45; DB 1; Length 770;
 Best Local Similarity 70.0%; Pred. No. 4;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 SMITMWYEDV 10
 :||:|||||
 DB 302 AMISRWYEDV 311

RESULT 7

JH0773
 Alzheimer's disease amyloid beta protein precursor - African clawed frog
 C:Species: Xenopus laevis (African clawed frog)
 C>Date: 10-Jun-1993 #sequence_revision 10-Jun-1993 #text_change 13-Aug-1999
 C:Accession: JH0773
 R:Okado, H.; Okamoto, H.
 Biochem. Biophys. Res. Commun. 189, 1561-1568, 1992
 A:Title: A Xenopus homologue of the human beta-amyloid precursor protein: developmental
 A:Reference number: JH0773; MUID:93129227
 A:Accession: JH0773
 A:Molecule type: mRNA
 A:Residues: 1-747 <OK>
 A:Cross-references: GB:S52417; NID:9263150; PIDN:AB24853.1; PID:9263151
 A:Experimental source: larva
 C:Superfamily: Alzheimer's disease amyloid beta protein; animal kunitz-type proteinase
 C:Keywords: alternative splicing; amyloid
 F:15-100/Domain: animal kunitz-type proteinase inhibitor homology <BPI>

Query Match 72.4% Score 42; DB 2; Length 747;
 Best Local Similarity 60.0%; Pred. No. 13;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 SMITMWYEDV 10
 :||:|||||
 DB 298 AMISRWYEDV 307

RESULT 8

PT0383
 Ig heavy chain V region (S107/VH11 group 2-27) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
 C:Accession: PT0383
 R:Behar, S.M.; Lustgarten, D.L.; Corbet, S.; Scharff, M.D.
 J. Exp. Med. 173, 731-741, 1991
 A:Title: Characterization of somatically mutated S107 VH11-encoded anti-DNA autoantibody
 A:Reference number: PT0376; MUID:91147903
 A:Accession: PT0383
 A:Molecule type: DNA
 A:Residues: 1-123 <BEH>
 C:Superfamily: Immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:15-100/Domain: immunoglobulin homology <IMM>

Query Match 70.7% Score 41; DB 2; Length 123;
 Best Local Similarity 60.0%; Pred. No. 2.8;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 SMITMWYEDV 10
 :||:|||||
 DB 102 ALXRMWYEDV 111

RESULT 9

PT0385
 Ig heavy chain V region (S107/VH11 group 2-2) - mouse (fragment)
 C:Species: Mus musculus (house mouse)

C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
 C:Accession: PT0385
 R:Behar, S.M.; Lustgarten, D.L.; Corbet, S.; Scharff, M.D.
 J. Exp. Med. 173, 731-741, 1991
 A:Title: Characterization of somatically mutated S107 VH11-encoded anti-DNA autoantibody
 A:Reference number: PT0376; MUID:91147903
 A:Accession: PT0385
 A:Molecule type: DNA
 A:Residues: 1-123 <BEH>
 C:Superfamily: Immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:15-100/Domain: immunoglobulin homology <IMM>

Query Match 70.7% Score 41; DB 2; Length 123;
 Best Local Similarity 60.0%; Pred. No. 2.8;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 SMITMWYEDV 10
 :||:|||||
 DB 102 ALXRMWYEDV 111

RESULT 10

PH1019
 Ig heavy chain V region (clone 165.33) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
 C:Accession: PH1019
 R:Fillman, D.M.; Jou, N.T.; Hill, R.J.; Matton, T.N.
 J. Exp. Med. 176, 761-779, 1992
 A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective
 A:Reference number: PH0971; MUID:92381444
 A:Accession: PH1019
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-111 <TIL>
 A:Experimental source: B cell, strain (NZB x NZW)F1
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:15-97/Domain: immunoglobulin homology <IMM>

Query Match 69.0% Score 40; DB 2; Length 111;
 Best Local Similarity 100.0%; Pred. No. 3.7;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 NMWYEDV 10
 :|||||
 DB 105 NMWYEDV 110

RESULT 11

A32530
 Ig heavy chain V region (DB3) - mouse
 C:Species: Mus musculus (house mouse)
 C>Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 21-Jan-2000
 C:Accession: A32530
 R:Deverson, E.; Bereh, C.; Taussig, M.; Feinstein, A.
 Eur. J. Immunol. 17, 9-13, 1987
 A:Title: Monoclonal BALB/c anti-progesterone antibodies use family IX variable region
 A:Reference number: A32530; MUID:87133855
 A:Accession: A32530
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-118 <DEV>
 A:Cross-references: GB:M27583
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:15-97/Domain: immunoglobulin homology <IMM>

Query Match 69.0% Score 40; DB 2; Length 118;

Best Local Similarity 100.0%; Pred. No. 4;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 NWYFDV 10
| | | | |
Db 102 NWYFDV 107

RESULT 12

PT0387
Ig heavy chain V region (S107/VH11 group 2-19) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C:Accession: PT0387
R:Behar, S.M.; Lustgarten, D.L.; Corbet, S.; Scharff, M.D.
J. Exp. Med. 173, 731-741, 1991
A:Title: Characterization of somatically mutated S107 VH11-encoded anti-DNA autoantibody
A:Reference number: PT0376; MUID:91147903
A:Accession: PT0387
A:Molecule type: DNA
A:Residues: 1-123 <BEH>
C:Superfamily: Immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-100/Domain: immunoglobulin homology <IMM>

Query Match 69.0%; Score 40; DB 2; Length 123;
Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 NWYFDV 10
| | | | |
Db 106 NWYFDV 111

RESULT 13

PT0386
Ig heavy chain V region (S107/VH11 group 2-17) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C:Accession: PT0386
R:Behar, S.M.; Lustgarten, D.L.; Corbet, S.; Scharff, M.D.
J. Exp. Med. 173, 731-741, 1991
A:Title: Characterization of somatically mutated S107 VH11-encoded anti-DNA autoantibody
A:Reference number: PT0376; MUID:91147903
A:Accession: PT0386
A:Molecule type: DNA
A:Residues: 1-123 <BEH>
C:Superfamily: Immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-100/Domain: immunoglobulin homology <IMM>

Query Match 69.0%; Score 40; DB 2; Length 123;
Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 NWYFDV 10
| | | | |
Db 106 NWYFDV 111

RESULT 14

A71533
Probable phospholipase D [imported] - Chlamydia trachomatis (serotype D, strain UW3/Cx)
C:Species: Chlamydia trachomatis
C:Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 04-Feb-2000
C:Accession: A71533
R:Stephens, R.S.; Kaiman, S.; Lammell, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell, Science 282, 754-759, 1998
A:Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trachomatis
A:Reference number: A71570; MUID:99000809
A:Accession: A71533

A>Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-474 <ARN>
A:Cross-references: GB:AE001301; GB:AE001273; NID:g3328697; PIDN:AA67877.1; PID:g332
A:Experimental source: serotype D, strain UW-3/Cx
C:Genetics:
A:Gene: CT284

Query Match 67.2%; Score 39; DB 2; Length 474;
Best Local Similarity 85.7%; Pred. No. 26;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 ITNMYFD 9
| | | | |
Db 452 ITNMYFD 458

RESULT 15

H81688
phospholipase D family protein TC0557 [imported] - Chlamydia muridarum (strain N19g)
C:Species: Chlamydia muridarum, Chlamydia trachomatis MOPn
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 11-May-2000
C:Accession: H81688
R:Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, C.; Dodson, R.; Gwin, M.; Nelson, W.; Deboy, R.; Kolonay, J.; McClarty, G.; Salzberg, E.S.; et al. Nucleic Acids Res. 28, 1397-1406, 2000
A:Title: Genome sequences of Chlamydia trachomatis MOPn and Chlamydia pneumoniae AR39
A:Reference number: AB1500; MUID:20150255
A:Accession: H81688
A>Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-474 <TEP>
A:Cross-references: GB:AE002324; GB:AE002160; NID:g7190597; PIDN:AAF39396.1; PID:g719
A:Experimental source: strain N19g (MOPn)
C:Genetics:
A:Gene: TC0557

Query Match 67.2%; Score 39; DB 2; Length 474;
Best Local Similarity 85.7%; Pred. No. 26;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 ITNMYFD 9
| | | | |
Db 452 ITNMYFD 458

Search completed: February 20, 2002, 12:16:20
Job time: 71 sec

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